

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1912

CCATAACCAT GAGTGATAAC AC

22

10

2) INFORMATION FOR SEQ ID NO: 1913

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1913

CGCCTTGATC ATTGGAACC

20

25

2) INFORMATION FOR SEQ ID NO: 1914

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1914

CGCCTTGATC GTTGAACC

20

40

2) INFORMATION FOR SEQ ID NO: 1915

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1915

CGCCTTGATA GTTGGGAACC

20

5

2) INFORMATION FOR SEQ ID NO: 1916

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1916

CGTGGGTCTT GCGGTATCAT

20

20

2) INFORMATION FOR SEQ ID NO: 1917

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1917

CGTGGGTCTG GCGGTATCAT

20

35

2) INFORMATION FOR SEQ ID NO: 1918

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 21 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1918

GTGGGTCTCA CGGTATCATT G

21

50

## 2) INFORMATION FOR SEQ ID NO: 1919

- (i) SEQUENCE CHARACTERISTICS:  
5 (A) LENGTH: 21 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1919

CGTGGGTCTC TCGGTATCAT T

21

15

## 2) INFORMATION FOR SEQ ID NO: 1920

- 20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1920

CGTGGNTCTC GCGGTATCAT

20

30

## 2) INFORMATION FOR SEQ ID NO: 1921

- 35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1921

45 CGTGGGTCTA GCGGTATCAT T

21

50

## 2) INFORMATION FOR SEQ ID NO: 1922

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 bases  
(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1922

GTTTTCCAAT GATTAGCACT TTTA

24

10

2) INFORMATION FOR SEQ ID NO: 1923

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1923

GTTTTCCAAT GATAAGCACT TTTA

24

25

2) INFORMATION FOR SEQ ID NO: 1924

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1924

GTTTTCCAAT GCTGAGCACT TTT

23

40

2) INFORMATION FOR SEQ ID NO: 1925

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1925

CGTTTTCCAA TGATGAGCAC TTT

23

5

2) INFORMATION FOR SEQ ID NO: 1926

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1926

GTTTTCCAAT GGTGAGCACT TTT

23

20

2) INFORMATION FOR SEQ ID NO: 1927

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 861 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 35 (A) ORGANISM: *Neisseria meningitidis*  
(B) STRAIN: MC9690-129  
(C) ACCESSION NUMBER: AF126482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1927

40	ATGAGTATTC AACATTTTCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT	50
	TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG	100
	CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAACT GGATCTCAAC	150
	AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT	200
	GAGCACTTTT AAAGTTCTGC TATGTGGTGC GGTATTATCC CGTGTTGACG	250
45	CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG	300
	GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT	350
	AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCTGCCA	400
	ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTG	450
	CACAACATGG GGGATCATGT AACTCGCCTT GATCGTTGGG AACCGGAGCT	500
50	GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA	550
	TGGCAACAAC GTTGCGCAAA CTATTAAGTG GCGAACTACT TACTCTAGCT	600
	TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC	650
	ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG	700

GAGCCGGTGA	GCGTGGGTCT	CGCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ACGACGGGGA	GTCAGGCAAC	800
TATGGATGAA	CGAAATAGAC	AGATCGCTGA	GATAGGTGCC	TCACTGATTA	850
AGCATTGGTA	A				861

5

## 2) INFORMATION FOR SEQ ID NO: 1928

## 10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: HB251
- (C) ACCESSION NUMBER: X57972

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1928

25	ATGAGTATTC	AACATTTCCG	TGTCGCCCTT	ATTCCCTTTT	TTGCGGCATT	50
	TTGCCTTCCT	GTTTTTGCTC	ACCCAGAAAC	GCTGGTGAAA	GTAAAAGATG	100
	CTGAAGATCA	GTTGGGTGCA	CGAGTGGGTT	ACATCGAACT	GGATCTCAAC	150
	AGCGGTAAGA	TCCTTGAGAG	TTTTCGCCCC	GAAGAACGTT	TTCCAATGAT	200
	GAGCACTTTT	AAAGTTCTGC	TATGTGGCGC	GGTATTATCC	CGTGTTGACG	250
30	CCGGGCAAGA	GCAACTCGGT	CGCCGCATAC	ACTATTCTCA	GAATGACTTG	300
	GTTAAGTACT	CACCAGTCAC	AGAAAAGCAT	CTTACGGATG	GCATGACAGT	350
	AAGAGAATTA	TGCAGTGCTG	CCATAACCAT	GAGTGATAAC	ACTGCGGCCA	400
	ACTTACTTCT	GACAACGATC	GGAGGACCGA	AGGAGCTAAC	CGCTTTTTTG	450
	CACAACATGG	GGGATCATGT	AACTCGCCTT	GATCATTGGG	AACCGGAGCT	500
35	GAATGAAGCC	ATACCAAACG	ACGAGCGTGA	CACCACGATG	CCTGCAGCAA	550
	TGGCAACAAC	GTTGCGCAAA	CTATTAAC TG	GCGAACTACT	TACTCTAGCT	600
	TCCCGGCAAC	AATTAATAGA	CTGGATGGAG	GCGGATAAAG	TTGCAGGACC	650
	ACTTCTGCGC	TCGGCCCTTC	CGGCTGGCTG	GTTTATTGCT	GATAAATCTG	700
	GAGCCGGTGA	GCGTGGGTCT	CGCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
40	GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ACGACGGGGA	GTCAGGCAAC	800
	TATGGATGAA	CGAAATAGAC	AGATCGCTGA	GATAGGTGCC	TCACTGATTA	850
	AGCATTGGTA	A				861

45

## 2) INFORMATION FOR SEQ ID NO: 1929

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Klebsiella oxytoca*  
 (B) STRAIN: 26W  
 (C) ACCESSION NUMBER: U09188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1929

```

10 ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT      50
   TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG      100
   CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAGCT GGATCTCAAC      150
   AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT      200
   GAGCACTTTT AAAGTTCTGC TATGTGGTGC GGTATTATCC CGTGTTGACG      250
15 CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG      300
   GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT      350
   AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCGGCCA      400
   ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTG      450
   CACAACATGG GGGATCATGT AACCCGCCCT GATAGTTGGG AACCGGAGCT      500
20 GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA      550
   TGGCAACAAC GTTGCGCAAA CTATTAAGTG GCGAACTACT TACTCTAGCT      600
   TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC      650
   ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG      700
   GAGCCGGTAA GCGTGGATCT CGCGGTATCA TTGCAGCACT GGGGCCAGAT      750
25 GGTAAGCCCT CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC      800
   TATGGATG                                     808
  
```

30 2) INFORMATION FOR SEQ ID NO: 1930

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases  
 (B) TYPE: Nucleic acid  
 35 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*  
 (C) ACCESSION NUMBER: AF190692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1930

```

45 ATGAGTATTC AACATTTTCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT      50
   TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG      100
   CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAACT GGATCTCAAC      150
   AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT      200
50 GAGCACTTTT AAAGTTCTGC TATGTGGCGC GGTATTATCC CGTGTTGACG      250
   CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG      300
   GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT      350
   AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCTGCCA      400
  
```

```

      ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTTG      450
      CACAACATGG GGGATCATGT AACTCGCCTT GATCGTTGGG AACCGGAGCT      500
      GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA      550
      TGGCAACAAC GTTGCGCAAA CTATTAAGTG GCGAACTACT TACTCTAGCT      600
5     TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC      650
      ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG      700
      GAGCCGGTGA GCGTGGGTCT GCGGTATCA TTGCAGCACT GGGGCCAGAT      750
      GGTAAGCCCT CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC      800
      TATGGATGAA CGAAATAGAC AGATCGCTGA GATAGGTGCC TCACTGATTA      850
10    AGCATTGGTA A                                         861

```

## 2) INFORMATION FOR SEQ ID NO: 1931

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

20

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

25

- (A) ORGANISM: *Escherichia coli*  
 (B) STRAIN: BM2728  
 (C) ACCESSION NUMBER: AF104442

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1931

30

```

      ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT      50
      TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG      100
      CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAACT GGATCTCAAC      150
      AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT      200
35    GAGCACTTTT AAAGTTCTGC TATGTGGCGC GGTATTATCC CGTGTTGACG      250
      CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG      300
      GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT      350
      AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCGGCCA      400
      ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTTG      450
40    CACAACATGG GGGATCATGT AACTCGCCTT GATCGTTGGG AACCGGAGCT      500
      GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA      550
      TGGCAACAAC GTTGCGCAAA CTATTAAGTG GCGAACTACT TACTCTAGCT      600
      TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC      650
      ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG      700
45    GAGCCGGTGA GCGTGGGTCT CTCGGTATCA TTGCAGCACT GGGGCCAGAT      750
      GGTAAGCCCT CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC      800
      TATGGATGAA CGAAATAGAC AGATCGCTGA GATAGGTGCC TCACTGATTA      850
      AGCATTGGTA A                                         861

```

50

## 2) INFORMATION FOR SEQ ID NO: 1932

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 5 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Escherichia coli*  
 (C) ACCESSION NUMBER: AF190695

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1932

```

15 ATGAGTATTC AACATTTTCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT      50
   TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG      100
   CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAACT GGATCTCAAC      150
   AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGCT      200
   GAGCACTTTT AAAGTTCTGC TATGTGGTGC GGTATTATCC CGTGTTGACG      250
20 CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG      300
   GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT      350
   AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCTGCCA      400
   ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTG      450
   CACAACATGG GGGATCATGT AACTCGCCTT GATCGTTGGG AACCGGAGCT      500
25 GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA      550
   TGGCAACAAC GTTGCGCAAA CTATTAAGTG GCGAACTACT TACTCTAGCT      600
   TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC      650
   ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG      700
   GAGCCGGTGA GCGTGGGTCT AGCGGTATCA TTGCAGCACT GGGGCCAGAT      750
30 GGTAAGCCCT CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC      800
   TATGGATGAA CGAAATAGAC AGATCGCTGA GATAGGTGCC TCACTGATTA      850
   AGCATTGGTA A                                     861

```

35

## 2) INFORMATION FOR SEQ ID NO: 1933

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases  
 40 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

45

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*  
 (C) ACCESSION NUMBER: AF190693

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1933

```

ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT      50
TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG      100

```

CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAGCT GGATCTCAAC 150  
AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGGT 200  
GAGCACTTTT AAAGTTCTGC TATGTGGTGC GGTATTATCC CGTGTTGACG 250  
CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG 300  
5 GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT 350  
AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCGGCCA 400  
ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTG 450  
CACAACATGG GGGATCATGT AACCCGCCTT GATCGTCGGG AACCGGAGCT 500  
GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA 550  
10 TGGCAACAAC GTTGCGCAAA CTATTAAGT GCGAACTACT TACTCTAGCT 600  
TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC 650  
ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG 700  
GAGCCGGTGA GCGTGGATCT CGCGGTATCA TTGCAGCACT GGGGCCAGAT 750  
GGTAAGCCCT CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC 800  
15 TATGGATGAA CGAGATAGAC AGATCGCTGA GATAGGTGCC TCACTGATTA 850  
AGCATTGGTA A 861

20 2) INFORMATION FOR SEQ ID NO: 1934

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases  
(B) TYPE: Nucleic acid  
25 (C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1934

GAACGCCAGC GCGAAATTCA AAAAG

25

35

2) INFORMATION FOR SEQ ID NO: 1935

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases  
40 (B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1935

AGCTCGGCAT ACTTCGACAG G

21

50

2) INFORMATION FOR SEQ ID NO: 1936

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 15 bases  
    (B) TYPE: Nucleic acid  
    (C) STRANDEDNESS: Single  
5      (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1936  
10      TACCACCCGC ACGGC 15
- 15   2) INFORMATION FOR SEQ ID NO: 1937
- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 bases  
    (B) TYPE: Nucleic acid  
20      (C) STRANDEDNESS: Single  
    (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 25   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1937  
    CGGAGTCGCC GTCGATG 17
- 30   2) INFORMATION FOR SEQ ID NO: 1938
- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 41 bases  
35      (B) TYPE: Nucleic acid  
    (C) STRANDEDNESS: Single  
    (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 40   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1938  
    CCGCGCACCA TTGCTTCGTA CACTGAGGAG TCTCCGCGCG G 41
- 45   2) INFORMATION FOR SEQ ID NO: 1939
- (i) SEQUENCE CHARACTERISTICS:  
50      (A) LENGTH: 46 bases  
    (B) TYPE: Nucleic acid  
    (C) STRANDEDNESS: Single  
    (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1939

5

CGACCCGGAT GGTAGTATCG ATAATGATCC GCCAGCGGCC GGGTCG

46

10 2) INFORMATION FOR SEQ ID NO: 1940

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: Nucleic acid

15 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1940

GTATCGTTGG TGACGTAAT

19

25

2) INFORMATION FOR SEQ ID NO: 1941

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases

30 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1941

GCAATGGTCC GTTTAAGT

18

40

2) INFORMATION FOR SEQ ID NO: 1942

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 27 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1942



GACTGGAACA AAGCCTATAA AAAATCA

27

## 5 2) INFORMATION FOR SEQ ID NO: 1943

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1943

GCTGGTGGAC GGCCAG

16

20

## 2) INFORMATION FOR SEQ ID NO: 1944

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- 25 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1944

TTTCGCCGCC ATGCGTTAC

19

35

## 2) INFORMATION FOR SEQ ID NO: 1945

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## 45 (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1945

CGGCGACTAC GCGGTAT

17

50

## 2) INFORMATION FOR SEQ ID NO: 1946

1013

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 bases  
    (B) TYPE: Nucleic acid  
5      (C) STRANDEDNESS: Single  
    (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 10      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1946  
  
CGGCGACTTC GCGGTAT 17
- 15      2) INFORMATION FOR SEQ ID NO: 1947
- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 19 bases  
20      (B) TYPE: Nucleic acid  
    (C) STRANDEDNESS: Single  
    (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 25      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1947  
  
CGGTATACGG CACCATCGT 19
- 30      2) INFORMATION FOR SEQ ID NO: 1948
- (i) SEQUENCE CHARACTERISTICS:  
35      (A) LENGTH: 19 bases  
    (B) TYPE: Nucleic acid  
    (C) STRANDEDNESS: Single  
    (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 40      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1948  
  
GCGGTATACA ACACCATCG 19
- 45      2) INFORMATION FOR SEQ ID NO: 1949
- 50      (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 19 bases  
    (B) TYPE: Nucleic acid  
    (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1949

CGGTATACGC CACCATCGT

19

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2) INFORMATION FOR SEQ ID NO: 1950

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 15 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1950

GGCGACATCG CCTGC

15

25

2) INFORMATION FOR SEQ ID NO: 1951

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 17 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1951

GGCGACAGAG CCTGCTA

17

40

2) INFORMATION FOR SEQ ID NO: 1952

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 19 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1952

CCTGCTATGG AGCGATGGT

19

5

## 2) INFORMATION FOR SEQ ID NO: 1953

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1953

CGCCTGCTAT AAAGCGATGG T

21

20

## 2) INFORMATION FOR SEQ ID NO: 1954

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*  
 (B) STRAIN: ATCC 13883  
 (C) ACCESSION NUMBER: AF052258

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1954

	ACACCGGTCA	ACATTGAGGA	AGAGCTTAAG	AACTCTTATC	TGGATTATGC	50
10	GATGTCGGTC	ATTGTTGGCC	GTGCGCTGCC	GGATGTCCGA	GATGGCCTGA	100
	AGCCGGTACA	CCGTCGCGTA	CTTTACGCCA	TGAACGTATT	GGGCAATGAC	150
	TGGAACAAAG	CCTATAAAAA	ATCAGCCCGT	GTCGTTGGTG	ACGTAATCGG	200
	TAAATACCAC	CCGCACGGCG	ACTCCGCGGT	ATACGACACC	ATCGTGCGTA	250
	TGGCGCAGCC	GTTCTCGCTG	CGTTACATGC	TGGTGGACGG	CCAGGGTAAC	300
15	TTTGGTTCCA	TCGACGGCGA	CTCCGCCGCG	GCGATGCGTT	ATACCGAAAT	350
	TCGTCTGGCG	AAAATCGCTC	ATGAGCTGAT	GGCCGATCTT	GAAAAAGAGA	400
	CGGTCGATTT	CGTCGACAAC	TATGACGGTA	CGGAGCGTAT	TCCGGACGTC	450
	ATGCCGACCA	AAATTCCTAA	CCTGCTGGTG	AACGGCGCCT	CCGGGATCGC	500
	CGTAGGGGATG	GCCACCAACA	TACCGCCACA	TAACCTGACG	GAAGTGATTA	550
20	ACGGCTGTCT	GGCGTATGTT	GACGATGAAG	ACATCAGCA		589

## 2) INFORMATION FOR SEQ ID NO: 1955

- (i) SEQUENCE CHARACTERISTICS:
- 5 (A) LENGTH: 38 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA  
10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1955

CGCGCAACCA TTGCTTCGTA CACTGAGGAG TCTGCGCG

38

15

## 2) INFORMATION FOR SEQ ID NO: 1956

- (i) SEQUENCE CHARACTERISTICS:
- 20 (A) LENGTH: 989 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida inconspicua*  
(B) STRAIN: ATCC 16783

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1956

	CGGTAAACC	ACTTTAACTG	CTGCAATCAC	CAAAGTTTTA	TCTGAAGAAG	50
	GTGGTGCAGA	TTTCTTAGAT	TATTCATCTA	TTGATAAAGC	ACCAGAAGAG	100
35	AGAGCTAGAG	GTATTACCAT	TTCTACTGCT	CATGTTGAAT	ATGAAACTCC	150
	AAACAGACAT	TATTCACATG	TTGATTGTCC	AGGTCATCAA	GATTATATTA	200
	AGAACATGAT	TACTGGTGCA	GCTCAAATGG	ATGGTGCTAT	TATTGTTGTT	250
	GCAGCTACTG	ATGGTCAAAT	GCCACAAACT	AAGGAACATT	TATTATTAGC	300
	TAGACAAGTT	GGTGTTC AAC	ATTTAGTTGT	TTTTGTTAAC	AAGTGTGATA	350
40	CCGTTGATGA	TCCAGAAATG	TTRGAATTAG	TTGAAATGGA	AATGAGAGAA	400
	TTATTGACCG	AATATGGATT	YGATGGTGAT	AACACACCAG	TTATTATGGG	450
	TTCTGCATTA	ATGGCATTAG	AAGGTAAGAG	ACCAGAAGTT	GGTAAAGAAT	500
	CTATTGTTAA	GTTAATGGAA	GCTGTTGATA	CTTGATTCC	AACTCCACAA	550
	AGAGACTTAG	AAAAACCAT	CTTATTACCA	ATTGATGAAG	TTTTCTCTAT	600
45	TTCTGGTAGA	GGTACTGTTG	TTTCTGGTAC	TGTTGATAGA	GGTACATTAA	650
	AGAAGGGTGA	AGAAGTTGAA	ATTGTTGGTG	GTAAAGAAGG	TGTTATTAAG	700
	ACTACTGTTA	CCGGTATTGA	AATGTATCAC	AAGGAATTAG	ATCAAGCACA	750
	AGCTGGTGAT	ACTCCAGGTA	TTTTGTTAAG	AGGTGTTAAG	AGAGATCAAA	800
	TTGCAAGAGG	TCAAATTCTT	GCAAAGCCAG	GWTCTGTTAA	GGCATACAAG	850
50	AAGTTCTTAT	CATCATTATA	CATTTTAAAC	AAGGAAGAAG	GTGGTAGACA	900
	TACTCCATTT	TCTGAAAATT	ACAGACCTCA	AATGTACATT	AGAACTTCCA	950
	ATGTTAATGT	TACTTTGAAG	TTCCAGAAA	CTGAAGAAG		989

## 2) INFORMATION FOR SEQ ID NO: 1957

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 991 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

10

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida utilis*  
 (B) STRAIN: ATCC 22023

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1957

	GGTAAGACCA	CCCTTACTGC	CGCCATCACC	AAGTGCCTTG	CTGAGAAGGG	50
	AGGTGCCTCG	TTCTTGGA	CTACAGTGCC	ATCGACAAGG	CGCCAGAGG	100
	GAGCAAGAGG	TATCACCATC	TCCACTGCGC	ACGTTGAGTA	TGAAACTGCC	150
20	AACAGACACT	ACTCGCACGT	TGACTGTCCA	GGTCACGCTG	ATTACATCAA	200
	GAACATGATT	ACCGGTGCTG	CGCAGATGGA	CGGTGCTATC	ATTGTCGTTG	250
	CAGCCACTGA	CGGTCAGATG	CCACAGACCA	GAGAACACTT	GTTGCTTGCC	300
	AGACAAGTTG	GTGTCCAGCA	CATTGTTGTC	TTCGTCAACA	AGGTTGACAC	350
	CATCGACGAC	CCTGAGATGC	TTGAGCTTGT	TGAAATGGAG	ATGAGAGAGT	400
25	TGCTTACTTC	GTATGGATTT	GACGGTGATA	ACACCCAGT	TATCATGGGT	450
	TCTGCTTTGT	GTGCTTTGGA	AGGCCGTGAG	CCAGAGATTG	GTGCTAAGGC	500
	CATTGACAAG	TTGATGGAGG	CCATTGATGA	GTACATCCCA	ACTCCTCAGA	550
	GAGACCTGGA	AAAGCCATTC	YTGATGGGTG	TTGAAGACGT	GTTCTCGATC	600
	TCTGGTAGAG	GTACCGTTGT	CACRGGCCGT	GTTGAGCGTG	GTAACCTGAA	650
30	GAAAGGTGAT	GAAATTGAAC	TTGTTGGCTA	CAACAAGAAC	CCAATCAAGA	700
	CCACCGTCAC	CGGTATCGAA	ATGTTCAAGA	AGGAGTTGGA	ATCTGCCATG	750
	GCTGGTGACA	ACTGTGGTAT	CTTGTTGCGT	GGTATCAAGA	GAGATGACGT	800
	CAAGAGAGGT	ATGGTTGCTG	CTAAGCCAGG	CTCCGTCTCT	GCACACACCA	850
	AGTTCCTCGC	TTCCTTGTA	ATCCTGACRA	AGGAGGAAGG	TGGTCGTCAC	900
35	AGTGCCTTTG	CTGAGAACTA	CAGACCACAG	ATGTTTCATCA	GAACCGGAGA	950
	TGTCACCACC	ATCTTGACAT	GGCCAGAGGA	GCACGCTGAC	C	991

## 40 2) INFORMATION FOR SEQ ID NO: 1958

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 985 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida zeylanoides*  
 (B) STRAIN: ATCC 7351

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1958

	CGGTAAGACC	ACTTTGACCG	CCGCCATCAC	CAAGGTGTTG	AGCGCCAAAG	50
	GTGGTGCTTC	CTTCTTGAC	TACGGGTCCA	TCGACAGAGC	CCCTGAGGAG	100
5	AGAGCCAGAG	GTATTACTAT	CTCGACTGCC	CACGTTGAGT	ACGAGACCGA	150
	TAAGAGACAC	TACGCCCACG	TTGATTGCCC	TGGTCACGCT	GATTACATCA	200
	AGAACATGAT	CACTGGTGCC	GCCCAAATGG	ACGGTGCCAT	TATTGTCGTT	250
	GCTGCTTCTG	ATGGCCAAAT	GCCGCAGACC	AGAGAGCACT	TGTTGCTTGC	300
	CAGACAGGTT	GGTGTGCAGA	ACTTGGTGTG	GTTTGTTAAC	AAGGTGGACA	350
10	CCATCGACGA	CCCCGAAATG	TTGGAGTTGG	TGGAGATGGA	AATGAGAGAA	400
	TTGTTGACCC	ACTACGGCTT	TGACGGTGAC	AACACCCCTG	TCATCATGGG	450
	TTCGGCGTTG	TGTGCCTTGG	AAGACAGGCA	GCCTGAGATT	GGCGAGCAAG	500
	CCATCATGAA	GTTGTTGGAC	GCTGTCGACG	AGTACATTCC	CACTCCTCAG	550
	AGAGACTTGG	AGCAACCATT	TTTGATGCCC	GTTGAGGATG	TTTTCTCCAT	600
15	CTCTGGCAGA	GGTACTGTTG	TCACCGGTCG	TGTTGAGAGA	GGCTCATTGA	650
	AGAAGGGTGA	GGAGATTGAG	ATTGTTGGCG	ACTTCCCCAA	GCCCTTCAAG	700
	ACTACCGTCA	CCGGCATTGA	GATGTTCAAG	AAGGAGTTGG	ATGCCGCGAT	750
	GGCGGGCGAC	AACGCCGGGA	TCTTGTTGAG	AGGTGTCAAG	AGAGACGAGG	800
	TCTCGAGAGG	TATGGTTTTG	GCCAAGCCCG	GTA CTGTAC	TTCGCACACC	850
20	AAGGTGTTGG	CGTCGCTTTA	CATCTTGACC	AAAGAGGAAG	GTGGCCGCCA	900
	CTCGCCCTTT	GGTGAGAACT	ACAAGCCACA	GTTATTCATC	AGAACCCTCCG	950
	ATGTCACTGG	TACTTTGAGG	TTCCCCGCCG	GTGAG		985

25

## 2) INFORMATION FOR SEQ ID NO: 1959

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 973 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Candida catenulata*
  - (B) STRAIN: ATCC 10565
  - (C) ACCESSION NUMBER:

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1959

	CGGTAAGACC	ACCTTGACTG	CCGCCATCAC	CAAGGTTCTC	TCCGAGAAGG	50
	GTGGTGCCGA	CTTCTTGAC	TACGGTGCCA	TTGACAGAGC	CCCCGAGGAG	100
45	CGTGCCCGTG	GTATCACCAT	CTCCACTGCC	CACGTTGAGT	ACGAGACTGA	150
	CAACCGTCAC	TACGCCCACA	TTGACTGTCC	CGGTCACGCT	GATTACATCA	200
	AGAACATGAT	TACCGGTGCC	GCCCAGATGG	ACGGTGCCAT	TATTGTCCTT	250
	GCTGCTACTG	ACGGTGCCAT	GCCCCAGACC	CGCGAGCACT	TGCTTCTCGC	300
	CCGTCAGGTT	GGTATCCAGG	AATTGGTGTG	GTTTGTGAAC	AAGGTTGACA	350
50	CCATCGACGA	CCCCGAGATG	TTGGAGCTCG	TTGAGATGGA	GATCCGCGAG	400
	TTGTTGTCTG	AGTTCGGTTT	TGACGGTGAC	AACACCCCGG	TCATCATGGG	450
	TTCCGCTTTG	TGCGCTTTGG	AGGGCAAGCA	GCCCCGAGAT	GGTGAGCAGG	500
	CTATCACCAA	GTTGATGGCC	GCCGTTGACG	AGCACATCCC	CACCCCCCAG	550

CGTGA CTTGG AGCAGCCTTT CTTGATGCCT GTTGAGGGTG TTTTCTCTAT 600  
 CTCTGGCCGT GGTACCGTGG TGA CTTGGTAA GGTGCCCCGT GGTGTCCTCA 650  
 AGAAGGGTGA GGAGATTGAG ATTGTTGGCA ACTTTGACAA GCCCTACAAG 700  
 GTGA CTTGTA CTGGTATTGA GATGTTCAAG AAGGAGTTGG ACCAGGCCAT 750  
 5 GGCTGGTGAC AACGCCGGTA TCTTGTTCG TGGTGTCAAG CGTGACGAGG 800  
 TGTCTCGTGG TATGGTTTTG GCCAAGCCCC GCACTGTTGT CTCGCACAAG 850  
 AAGGTTTTGG CTTGCTTTA CATCTTGACC CAGGAGGAG GTGGCCGTAA 900  
 GACCGGCTTC GGCTCCAAC ACAAGCCCCA GTTGTTCCTG CGCACTACCG 950  
 ACGTCACTGG TACCCTCACC TTC 973  
 10

## 2) INFORMATION FOR SEQ ID NO: 1960

## 15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 985 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

20

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida krusei*  
 25 (B) STRAIN: ATCC 28870

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1960

AAGACTACCT TGA CTTGCTGC AATCACCAAG GTCTTAGCTG ATCAAGGTGG 50  
 30 TGCTGATTTT TTAGATTATG CATCTATTGA CAAGGCTCCT GAAGAAAGAG 100  
 CAAGAGGTAT TACTATCTCT ACTGCTCAG TTGAGTATGA AACCCCAAAC 150  
 AGACATTATT CTCATGTCGA TTGTCCTGGC CATCAAGATT ATATTAAGAA 200  
 TATGATTACT GGTGCTGCAC AAATGGATGG TGCTATTATT GTTGTGCTG 250  
 CTACTGATGG TCAAATGCCA CAACTAAGG AACATTTATT ATTAGCAAGA 300  
 35 CAAGTTGGTG TTCAACATTT AGTTGTCTTT GTTAATAAAT GTGACACCAT 350  
 TGATGACCCA GAAATGTTGG AATTAGTTGA AATGGAAATG AGAGAACTAT 400  
 TGTCTGAATA TGGTTTTGAT GGTGATAACA CTCCAGTTAT TATGGGTTCT 450  
 GCATTGATGG CTTTAGAAGA CAAGAGACCT GAAGTTGGTA AGGAATCTAT 500  
 TTTAAAGTTA ATGGAAGCYG TTGACACATG GATTCCAACC CCAGAGAGAG 550  
 40 ATTTAGAAAA ACCATTTTTG TTACCTATTG ATGAAGTTTT CTCAATCTCT 600  
 GGTAGAGGTA CTGTCGTTTC TGGTACTGTC GAAAGAGGTA CTTTGAAGAA 650  
 GGGTGAAGAA GTTGAAATTG TTGGTGGTAA GGATGGTTCT ATTAAACTA 700  
 CTGTCACAGG TATTGAAATG TATCACAAGG AATTAGACCA AGCGCAAGCA 750  
 GGTGATACTC CAGGTATTTT ATTAAGAGGT GTCAAGAGAG ACCAAATCAA 800  
 15 GAGAGGTCAA ATTTTAGCAA AGCCAGATTC CGTTAAGGCA TACAAGAAGT 850  
 TCTTGGCTTC CCTTTATATC TTAACCAAGG AAGAAGGTGG TAGACATACA 900  
 CCATTCTCTG AAAACTACAG ACCACAAATG TACATCAGAA CTACCAATGT 950  
 TAACGTTACT TTGAAGTTCC CAGACACTGA AGAAG 985

50

## 2) INFORMATION FOR SEQ ID NO: 1961



(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22 bases  
    (B) TYPE: Nucleic acid  
    (C) STRANDEDNESS: Single  
5      (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1961  
10      GCTCAAGGCA GATGGCATTC CC      22

15   2) INFORMATION FOR SEQ ID NO: 1962

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22 bases  
    (B) TYPE: Nucleic acid  
20      (C) STRANDEDNESS: Single  
    (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1962  
    GGACAAGGCG GTTGCGTTTG AT      22

30   2) INFORMATION FOR SEQ ID NO: 1963

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22 bases  
35      (B) TYPE: Nucleic acid  
    (C) STRANDEDNESS: Single  
    (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1963  
    CATCCCCGTC TCGCTCGACA GT      22

45   2) INFORMATION FOR SEQ ID NO: 1964

(i) SEQUENCE CHARACTERISTICS:  
50      (A) LENGTH: 19 bases  
    (B) TYPE: Nucleic acid  
    (C) STRANDEDNESS: Single  
    (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1964

5

ATCTGCCTGC CCGTCTTGC

19

10 2) INFORMATION FOR SEQ ID NO: 1965

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 816 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Plasmid pGS05  
(C) ACCESSION NUMBER: M36657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1965

25

ATGAATAAAT CGCTCATCAT TTTCGGCATC GTCAACATAA CCTCGGACAG 50  
TTTCTCCGAT GGAGGCCGGT ATCTGGCGCC AGACGCAGCC ATTGCGCAGG 100  
CGCGTAAGCT GATGGCCGAG GGGGCAGATG TGATCGACCT CCGTCCGGCA 150  
TCCAGCAATC CCGACGCCGC GCCTGTTTCG TCCGACACAG AAATCGCGCG 200  
30 TATCGCGCCG GTGCTGGACG CGCTCAAGGC AGATGGCATT CCCGTCTCGC 250  
TCGACAGTTA TCAACCCGCG ACGCAAGCCT ATGCCTTGTC GCGTGGTGTG 300  
GCCTATCTCA ATGATATTCG CGGTTTTCCA GACGCTGCGT TCTATCCGCA 350  
ATTGGCGAAA TCATCTGCCA AACTCGTCGT TATGCATTCG GTGCAAGACG 400  
GGCAGGCAGA TCGGCGCGAG GCACCCGCTG GCGACATCAT GGATCACATT 450  
35 GCGGCGTTCT TTGACGCGCG CATCGCGGCG CTGACGGGTG CCGGTATCAA 500  
ACGCAACCGC CTTGTCCTTG ATCCCGGCAT GGGGTTTTTT CTGGGGGGCTG 550  
CTCCCGAAAC CTCGCTCTCG GTGCTGGCGC GGTTCGATGA ATTGCGGCTG 600  
CGCTTCGATT TGCCGGTGCT TCTGTCTGTT TCGCGCAAAT CCTTTCTGCG 650  
CGCGCTCACA GGCCGTGGTC CGGGGGATGT CGGGGCCGCG ACACTCGCTG 700  
10 CAGAGCTTGC CGCCGCCGCA GGTGGAGCTG ACTTCATCCG CACACACGAG 750  
CCGCGCCCCT TGC GCGACGG GCTGGCGGTA TTGGCGGCGC TGAAAGAAAC 800  
CGCAAGAATT CGTTAA 816

15

2) INFORMATION FOR SEQ ID NO: 1966

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 19 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1966

5 CATGCCAGTC TTGCCAACG 19

2) INFORMATION FOR SEQ ID NO: 1967

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1967

20

CAGCAATAAG TAATCCAGCG ATG 23

25 2) INFORMATION FOR SEQ ID NO: 1968

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1968

GGAGAGATTT CACCGCATAG 20

40

2) INFORMATION FOR SEQ ID NO: 1969

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1969

AGCCAACCAT CATGCTATTC CA 22

## 2) INFORMATION FOR SEQ ID NO: 1970

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1206 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

10

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Transposon Tn10  
 (C) ACCESSION NUMBER: J01830

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1970

ATGAATAGTT CGACAAAGAT CGCATTGGTA ATTACGTTAC TCGATGCCAT 50  
 GGGGATTGGC CTTATCATGC CAGTCTTGCC AACGTTATTA CGTGAATTTA 100  
 TTGCTTCGGA AGATATCGCT AACCACCTTTG GCGTATTGCT TGCACCTTTAT 150  
 20 GCGTTAATGC AGGTTATCTT TGCTCCTTGG CTTGGAAAAA TGTCTGACCG 200  
 ATTTGGTCGG CGCCAGTGC TGTGTGTGTC ATTAATAGGC GCATCGCTGG 250  
 ATTACTTATT GCTGGCTTTT TCAAGTGCGC TTTGGATGCT GTATTTAGGC 300  
 CGTTTGCTTT CAGGGATCAC AGGAGCTACT GGGGCTGTCG CGGCATCGGT 350  
 CATTGCCGAT ACCACCTCAG CTTCTCAACG CGTGAAGTGG TTCGGTTGGT 400  
 25 TAGGGGCAAG TTTTGGGCTT GGTTTAATAG CGGGGCCTAT TATTGGTGGT 450  
 TTTGCAGGAG AGATTTCACC GCATAGTCCC TTTTTTATCG CTGCGTTGCT 500  
 AAATATTGTC ACTTTCCTTG TGGTTATGTT TTGGTTCCGT GAAACCAAAA 550  
 ATACACGTGA TAATACAGAT ACCGAAGTAG GGGTTGAGAC GCAATCGAAT 600  
 TCGGTATACA TCACTTTATT TAAAACGATG CCCATTTTGT TGATTATTTA 650  
 30 TTTTTCAGCG CAATTGATAG GCCAAATTCC CGCAACGGTG TGGGTGCTAT 700  
 TTACCGAAAA TCGTTTGGGA TGGAATAGCA TGATGGTTGG CTTTTCATTA 750  
 GCGGGTCTTG GTCTTTTACA CTCAGTATTC CAAGCCTTTG TGGCAGGAAG 800  
 AATAGCCACT AAATGGGGCG AAAAAACGGC AGTACTGCTC GAATTTATTG 850  
 CAGATAGTAG TGCATTTGCC TTTTATGCGT TTATATCTGA AGGTTGGTTA 900  
 35 GATTTCCCTG TTTTAATTTT ATTGGCTGGT GGTGGGATCG CTTTACCTGC 950  
 ATTACAGGGA GTGATGTCTA TCCAAACAAA GAGTCATGAG CAAGGTGCTT 1000  
 TACAGGGATT ATTGGTGAGC CTTACCAATG CAACCGGTGT TATTGGCCCA 1050  
 TTAAGTTTGA CTGTTATTTA TAATCATTCA CTACCAATTT GGGATGGCTG 1100  
 GATTTGGATT ATTGGTTTAG CGTTTACTG TATTATTATC CTGCTATCGA 1150  
 40 TGACCTTCAT GTTAACCCCT CAAGCTCAGG GGAGTAAACA GGAGACAAGT 1200  
 GCTTAG 1206

## 15 2) INFORMATION FOR SEQ ID NO: 1971

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 21 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1971

5 CYGACTGYGC CATCCTYATC A

21

2) INFORMATION FOR SEQ ID NO: 1972

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 21 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1972

20 MGICAGCTCA TYITTGCWKS C

21

2) INFORMATION FOR SEQ ID NO: 1973

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1973

35 RACACCRGIY TTGGWITCCT T

21

2) INFORMATION FOR SEQ ID NO: 1974

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1974

50 ACAAGGGITG GRMSAAGGAG AC

22

## 2) INFORMATION FOR SEQ ID NO: 1975

- (i) SEQUENCE CHARACTERISTICS:  
5 (A) LENGTH: 21 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1975

15 TGRCCRGGGT GGTTRAGGAC G

21

## 2) INFORMATION FOR SEQ ID NO: 1976

- 20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1976

30 GATGGAYTCY GTYAAITGGG A

21

## 2) INFORMATION FOR SEQ ID NO: 1977

- 35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
10 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1977

15 GATGGAYTCY GTYAARTGGG A

21

## 2) INFORMATION FOR SEQ ID NO: 1978

- 50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1978

CATCITGYAA TGGYAATCTY AAT

23

10

2) INFORMATION FOR SEQ ID NO: 1979

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1979

CATCYTGYAA TGGYAASCTY AAT

23

25

2) INFORMATION FOR SEQ ID NO: 1980

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1980

40 TCRATGGCIT CIAIRAGRGT YT

22

2) INFORMATION FOR SEQ ID NO: 1981

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1981

TGGACACCIS CAAGIGGKCY G

21

5

2) INFORMATION FOR SEQ ID NO: 1982

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 21 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1982

TGGACACYIS CAAGIGGKCY G

21

20

2) INFORMATION FOR SEQ ID NO: 1983

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 21 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1983

35 CYGAYTGCGC YATICTCATC A

21

2) INFORMATION FOR SEQ ID NO: 1984

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 21 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1984

50

CYGAYTGYGC YATYCTSATC A

21



## 2) INFORMATION FOR SEQ ID NO: 1985

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1383 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptococcus neoformans*  
 (B) STRAIN: M1-106  
 (C) ACCESSION NUMBER: U81804

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1985

	ATGGGTAAGG	ACAAGCTGCA	CGTCAACGTC	GTTGTTATCG	GTCACGTCGA	50
	CTCCGGTAAG	TCGACCACCA	CCGGTCACTT	GATCTACAAG	TGCGGTGGTA	100
20	TCGACAAGCG	AACCATTGAG	AAGTTCGAGA	AGGAGGCTCA	AGAGCTCGGA	150
	AAGTCTTCTT	TCAAGTACGC	TTGGGTTCCT	GACAAGCTTA	AGGCCGAGCG	200
	AGAGCGAGGT	ATCACCATCG	ACATTGCTCT	TTGGAAGTTC	GAGACCCCTA	250
	AGTACCAGGT	TACCGTCATT	GACGCCCCCG	GTCACCGAGA	CTTCATCAAG	300
	AACATGATCA	CCGGTACCTC	CCAGGCTGAC	TGTGCCATCC	TCATCATTCG	350
25	CACCGGTATC	GGTGAGTTCG	AGGCTGGTAT	CTCCAAGGAC	GGTCAGACCC	400
	GAGAGCACGC	CCTCCTCGCC	TTCACCCTCG	GTGTCAGGCA	GCTCATTGTT	450
	GCTTGCAACA	AGATGGACAC	CTGCAAGTGG	TCTGAGGACC	GATTCAACGA	500
	AATCGTCAAG	GAGACCAACG	GTTTCATCAA	GAAGGTTGGT	TACAACCCCA	550
	AGGCTGTCCC	CTTCGTCCCC	ATCTCTGGTT	GGCACGGTGA	CAACATGTTG	600
30	GAGGAGACCA	CCAACATGCC	CTGGTACAAG	GGATGGACCA	AGGAGACCAA	650
	GTCCGGTGTT	TCCAAGGGTA	AGACCCTTCT	CGAGGCCATC	GACGCCAGTA	700
	GGCCCCCTAC	CCGACCCACC	GACAAGCCCC	TCCGTCTCCC	TCTCCAGGAC	750
	GTCTACAAGA	TCGGTGGTAT	CGGCACAGTC	CCTGTCGGCC	GAGTCGAGAC	800
	CGGTGTCATC	AAGGCCGGTA	TGGTCGTCAA	GTTTCGCCCC	ACCAACGTCA	850
35	CCACTGAAGT	CAAGTCCGTT	GAGATGCACC	ACGAGCAGAT	CCCCGAGGGT	900
	CTCCCCGGAG	ACAACGTTGG	TTTCAACGTC	AAGAACGTTT	CCATCAAGGA	950
	CATCCGACGA	GGTAACGTCT	GTGGTGACTC	CAAGAACGAC	CCCCCTATGG	1000
	AGGCTGCTTC	TTTCAACGCC	CAGGTTATCG	TCCTTAACCA	CCCTGGTCAG	1050
	ATCGGTGCCG	GTTACACCCC	CGTTCTCGAC	TGTCACACTG	CCCACATTGC	1100
40	TTGCAAGTTC	TCTGAGTTGA	TCGAGAAGAT	TGACCGACGA	ACCGGTAAGG	1150
	TCATGGAGGC	CGCCCCCAAG	TTCGTCAAGT	CTGGTGACGC	CGCCATTGTC	1200
	AAGCTTGTTT	CCCAGAAGCC	TCTCTGTGTT	GAGACCTACG	CCGACTACCC	1250
	CCCTCTTGGT	CGATTGCGCG	TCCGAGACAT	GCGACAGACC	GTTGCCGTTG	1300
	GTGTTATTAA	GAGTGTGGAG	AAGTCCGATG	GGAAGAGCGG	CAAGGTTACC	1350
45	AAGGCCGCCG	AGAAGGCTGC	TAAGAAGAAG	TAA		1383

## 2) INFORMATION FOR SEQ ID NO: 1986

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1380 bases  
 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptococcus neoformans*  
(B) STRAIN: B3501  
(C) ACCESSION NUMBER: U81803

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1986

	ATGGGTAAGG	ACAAGCTGCA	CGTCAACGTC	GTTGTTATCG	GTCACGTCGA	50
	CTCCGGTAAG	TCGACCACCA	CCGGTCACTT	GATCTACAAG	TGCGGTGGTA	100
15	TCGACAAGCG	AACCATTGAG	AAGTTTCGAGA	AGGAGGCTCA	AGAGCTCGGA	150
	AAGTCTTCTT	TCAAGTACGC	TTGGGTTCCT	GACAAGCTTA	AGGCCGAGCG	200
	AGAGCGAGGT	ATCACCATCG	ACATTGCTCT	TTGGAAGTTC	GAGACCCCCA	250
	GGTACCAGGT	CACCGTCATT	GACGCCCCCG	GTCACCGAGA	CTTCATCAAG	300
	AACATGATCA	CCGGTACCTC	CCAGGCTGAC	TGTGCCATCC	TCATCATTCG	350
20	CACCGGTATC	GGTGAGTTCG	AGGCCGGTAT	CTCCAAGGAC	GGTCAGACCC	400
	GAGAGCACGC	CCTCCTCGCC	TTCACCCTCG	GTGTCAGGCA	GCTCATTTGT	450
	GCTTGCAACA	AGATGGACAC	CTGCAAGTGG	TCCGAGGACC	GATTCAACGA	500
	AATCGTCAAG	GAGACCAACG	GTTTCATCAA	GAAGGTTGGC	TACAACCCCCA	550
	AGGCTGTCCC	CTTCGTCCCC	ATCTCTGGTT	GGCACGGTGA	CAACATGTTG	600
25	GAGGAGACCA	CCAACATGCC	CTGGTACAAG	GGATGGACCA	AGGAGACCAA	650
	GTCTGGTGTG	TCCAGGGGTA	AGACCCTTCT	CGAGGCCATC	AGCGCCAGTA	700
	GGCCCCATAC	CCGACCCACC	GACAAGCCCC	TCCGTCTCCC	TCTCCAGGAC	750
	GTCTACAAGA	TCGGTGGTAT	CGGCACAGTC	CCTGTCGGCC	GAGTCGAGAC	800
	CGGTGTCATC	AAGGCCGGTA	TGGTCGTCAA	GTTTCGCCCC	ACCAACGTCA	850
30	CCACTGAAGT	CAAGTCCGTT	GAGATGCACC	ACGAGCAGAT	CCCCGAGGGT	900
	CTTCCCGGAG	ACAACGTTGG	TTTCAACGTC	AAGAACGTTT	CCATCAAGGA	950
	CATCCGACGA	GGTAACGTCT	GTGGTGACTC	CAAGAACGAC	CCCCCTATGG	1000
	AGGCTGCTTC	TTTCAACGCC	CAGGTTATCG	TCCTTAACCA	CCCTGGTCAG	1050
	ATCGGTGCCG	GTTACACCCC	CGTTCTCGAC	TGTCACACTG	CCCACATTGC	1100
35	CTGCAAGTTT	GCTGAGTTGA	TCGAGAAGAT	TGACCGACGA	ACCGGTAAGG	1150
	TCATGGAGGC	CGCCCCAAG	TTCGTCAAGT	CTGGTGACGC	CGCCATTGTC	1200
	AAGCTTGTTG	CCCAGAAGCC	CCTCTGTGTT	GAGACCTACG	CCGACTACCC	1250
	CCCTCTTGGT	CGATTGCGCG	TCCGAGACAT	GCGACAGACC	GTTGCCGTTG	1300
	GTGTTATCAA	GAGCGTGGAC	AAGACCGAGA	AGGGTGGCAA	GGTCACCAAG	1350
40	GCTGCTGAGA	AGGCTGCCAA	GAAGAAGTAA			1380

2) INFORMATION FOR SEQ ID NO: 1987

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1377 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(C) ACCESSION NUMBER: X01638

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1987

```

ATGGGTAAAG AGAAGTCTCA CATTACGTT GTCGTTATCG GTCATGTCGA      50
TTCTGGTAAG TCTACCACTA CCGGTCATTT GATTTACAAG TGTGGTGGTA      100
TTGACAAGAG AACCATCGAA AAGTTCGAAA AGGAAGCCGC TGAATTAGGT      150
10 AAGGGTTCTT TCAAGTACGC TTGGGTTTTG GACAAGTTAA AGGCTGAAAG      200
AGAAAGAGGT ATCACTATCG ATATTGCTTT GTGGAAGTTC GAAACTCCAA      250
AGTACCAAGT TACCGTTATT GATGCTCCAG GTCACAGAGA TTTCATCAAG      300
AACATGATTA CTGGTACTTC TCAAGCTGAC TGTGCTATCT TGATTATTGC      350
TGGTGGTGTC GGTGAATTCG AAGCCGGTAT CTCTAAGGAT GGTCAAACCA      400
15 GAGAACACGC TTTGTTGGCT TTCACCTTGG GTGTTAGACA ATTGATTGTT      450
GCTGTCAACA AGATGGACTC CGTCAAATGG GACGAATCCA GATTCCAAGA      500
AATTGTCAAG GAAACCTCCA ACTTTATCAA GAAGGTTGGT TACAACCCAA      550
AGACTGTTCC ATTCGTCCCA ATCTCTGGTT GGAACGGTGA CAACATGATT      600
GAAGCTACCA CCAACGCTCC ATGGTACAAG GGTGGGAAA AGGAAACCAA      650
20 GGCCGGTGTC GTCAAGGGTA AGACTTTGTT GGAAGCCATT GACGCCATTG      700
AACAACCATC TAGACCAACT GACAAGCCAT TGAGATTGCC ATTGCAAGAT      750
GTTTACAAGA TCGGTGGTAT TGGTACTGTG CCAGTCGGTA GAGTTGAAAC      800
CGGTGTCATC AAGCCAGGTA TGGTTGTTAC TTTCGCCCCA GCTGGTGTTA      850
CCACTGAAGT CAAGTCCGTT GAAATGCATC ACGAACAATT GGAACAAGGT      900
25 GTTCCAGGTG ACAACGTTGG TTTCAACGTC AAGAACGTTT CCGTTAAGGA      950
AATCAGAAGA GGTAACGTCT GTGGTGACGC TAAGAACGAT CCACCAAAGG     1000
GTTGCGCTTC TTTCAACGCT ACCGTCATTG TTTTGAACCA TCCAGGTCAA     1050
ATCTCTGCTG GTTACTCTCC AGTTTTGGAT TGTCACACTG CTCACATTGC     1100
TTGTAGATTC GACGAATTGT TGGAAAAGAA CGACAGAAGA TCTGGTAAGA     1150
30 AGTTGGAAGA CCATCCAAAG TTCTTGAAGT CCGGTGACGC TGCTTTGGTC     1200
AAGTTCGTTC CATCTAAGCC AATGTGTGTT GAAGCTTTCA GTGAATACCC     1250
ACCATTAGGT AGATTGCTG TCAGAGACAT GAGACAAACT GTCGCTGTGCG     1300
GTGTTATCAA GTCTGTTGAC AAGACTGAAA AGGCCGCTAA GGTTACCAAG     1350
GCTGCTCAAA AGGCTGCTAA GAAATAA                                     1377
35

```

## 2) INFORMATION FOR SEQ ID NO: 1988

## 40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1377 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

45

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

50 (C) ACCESSION NUMBER: M10992

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1988

	ATGGGTAAAG	AGAAGTCTCA	CATTAACGTT	GTCGTTATCG	GTCATGTCGA	50
	TTCTGGTAAG	TCTACCACTA	CCGGTCATTT	GATTTACAAG	TGTGGTGGTA	100
	TTGACAAGAG	AACCATCGAA	AAGTTCGAAA	AGGAAGCCGC	TGAATTAGGT	150
	AAGGGTTCTT	TCAAGTACGC	TTGGGTTTTG	GACAAGTTAA	AGGCTGAAAG	200
5	AGAAAGAGGT	ATCACTATCG	ATATTGCTTT	GTGGAAGTTC	GAAACTCCAA	250
	AGTACCAAGT	TACCGTTATT	GATGCTCCAG	GTCACAGAGA	TTTCATCAAG	300
	AACATGATTA	CTGGTACTTC	TCAAGCTGAC	TGTGCTATCT	TGATTATTGC	350
	TGGTGGTGTC	GGTGAATTCG	AAGCCGGTAT	CTCTAAGGAT	GGTCAAACCA	400
	GAGAACACGC	TTTGTTGGCT	TTCACCTTGG	GTGTTAGACA	ATTGATTGTT	450
10	GCTGTCAACA	AGATGGACTC	CGTCAAATGG	GACGAATCCA	GATTCCAAGA	500
	AATTGTCAAG	GAAACCTCCA	ACTTTATCAA	GAAGGTTGGT	TACAACCCAA	550
	AGACTGTTCC	ATTCGTCCCA	ATCTCTGGTT	GGAACGGTGA	CAACATGATT	600
	GAAGCTACCA	CCAACGCTCC	ATGGTACAAG	GGTTGGGAAA	AGGAAACCAA	650
	GGCCGGTGTC	GTCAAGGGTA	AGACTTTGTT	GGAAGCCATT	GACGCCATTG	700
15	AACAACCATC	TAGACCAACT	GACAAGCCAT	TGAGATTGCC	ATTGCAAGAT	750
	GTTTACAAGA	TTGGTGGTAT	TGGTACTGTG	CCAGTCGGTA	GAGTTGAAAC	800
	CGGTGTCATC	AAGCCAGGTA	TGGTTGTTAC	TTTTGCCCCA	GCTGGTGTTA	850
	CCACTGAAGT	CAAGTCCGTT	GAAATGCATC	ACGAACAATT	GGAACAAGGT	900
	GTTCCAGGTG	ACAACGTTGG	TTTCAACGTC	AAGAACGTTT	CCGTTAAGGA	950
20	AATCAGAAGA	GGTAACGTCT	GTGGTGACGC	TAAGAACGAT	CCACCAAAGG	1000
	GTTGCGCTTC	TTTCAACGCT	ACCGTCATTG	TTTTGAACCA	TCCAGGTCAA	1050
	ATCTCTGCTG	GTTACTCTCC	AGTTTTGGAT	TGTCACACTG	CTCACATTGC	1100
	TTGTAGATTC	GACGAATTGT	TGGAAAAGAA	CGACAGAAGA	TCTGGTAAGA	1150
	AGTTGGAAGA	CCATCCAAAG	TTCTTGAAGT	CCGGTGACGC	TGCTTTGGTC	1200
25	AAGTTCGTTC	CATCTAAGCC	AATGTGTGTT	GAAGCTTTCA	GTGAATACCC	1250
	ACCATTAGGT	AGATTGCTG	TCAGAGACAT	GAGACAAACT	GTCGCTGTCTG	1300
	GTGTTATCAA	GTCTGTTGAC	AAGACTGAAA	AGGCCGCTAA	GGTTACCAAG	1350
	GCTGCTCAAA	AGGCTGCTAA	GAAATAA			1377

30

## 2) INFORMATION FOR SEQ ID NO: 1989

- (i) SEQUENCE CHARACTERISTICS:
- 35 (A) LENGTH: 1377 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- 40 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Eremothecium gossypii*
- (B) STRAIN: ATCC 10895
- 45 (C) ACCESSION NUMBER: X73978

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1989

	ATGGGTAAGG	AAAAGACTCA	CGTTAACGTT	GTCGTCATCG	GTACAGTCGA	50
50	CTCTGGTAAG	TCTACTACCA	CCGGTCACTT	GATCTACAAG	TGTGGTGGTA	100
	TTGACAAGAG	AACCATCGAG	AAGTTCGAGA	AGGAGGCTGC	CGAGTTGGGT	150
	AAGGGTTCTT	TCAAGTACGC	CTGGGTTTTG	GACAAATTGA	AGGCTGAGAG	200
	AGAGAGAGGT	ATCACCATCG	ACATTGCGTT	GTGGAAGTTC	GAGACTCCAA	250

	AGTACCACGT	CACTGTCATT	GACGCCCCAG	GCCACAGAGA	CTTCATCAAG	300
	AACATGATTA	CCGGTACTTC	TCAAGCTGAC	TGTGCCATCT	TGATCATTGC	350
	TGGTGGTGTC	GGTGAGTTCG	AGGCTGGTAT	CTCCAAGGAC	GGTCAGACCA	400
	GAGAGCACGC	TTTGTTGGCT	TACACCTTGG	GTGTCAAGCA	GTTGATCGTT	450
5	GCCATCAACA	AGATGGACTC	CGTCAAGTGG	GACGAGTCCA	GATACCAGGA	500
	GATTGTCAAG	GAGACCTCCA	ACTTCATCAA	GAAGGTCGGT	TACAACCCTA	550
	AGACTGTTCC	ATTCGTTCCA	ATCTCCGGCT	GGAACGGTGA	CAACATGATT	600
	GAGGCCACCA	CCAACGCCCC	ATGGTACAAG	GGCTGGGAGA	AGGAGACCAA	650
	GGCTGGTGCC	GTCAAGGGTA	AGACCTTGTT	GGAGGCCATT	GACGCCATTG	700
10	AGCCACCTGT	CAGACCAACT	GACAAGGCAT	TGAGATTGCC	ATTGCAGGAT	750
	GTCTACAAGA	TCGGTGGTAT	TGGTACGGTT	CCAGTCGGCA	GAGTCGAGAC	800
	CGGTGTCATC	AAGCCAGGTA	TGGTTGTTAC	CTTCGCCCCA	TCCGGTGTCA	850
	CCACTGAAGT	CAAGTCCGTC	GAGATGCACC	ACGAGCAATT	GGAGGAGGGT	900
	GTCCCAGGTG	ACAACGTTGG	TTTCAACGTC	AAGAACGTCT	CCGTCAAGGA	950
15	GATCAGAAGA	GGTAACGTTT	GCGGTGACTC	CAAGAACGAC	CCACCAAAGG	1000
	CTGCTGAGTC	CTTCAACGCT	ACCGTCATTG	TCTTGAACCA	CCCAGGTCAA	1050
	ATCTCTGCCG	GTTACTCTCC	AGTCTTGGAC	TGTCACACTG	CCCACATTGC	1100
	TTGTAAGTTC	GACGAGTTGT	TGGAGAAGAA	CGACAGAAGA	ACCGGTAAGA	1150
	AGTTGGAAGA	CTCTCCAAAG	TTCCTAAAGG	CCGGTGACGC	TGCCATGGTC	1200
20	AAGTTTGTCC	CATCCAAGCC	AATGTGTGTT	GAGGCTTTCA	CCGACTACCC	1250
	ACCATTGGGT	AGATTGCTG	TCAGAGACAT	GAGACAGACC	GTTGCTGTCG	1300
	GTGTCATCAA	GTCTGTTGTC	AAGTCCGACA	AGGCTGGTAA	GGTCACCAAG	1350
	GCCGCCAAA	AGGCTGGTAA	GAAATAG			1377

25

## 2) INFORMATION FOR SEQ ID NO: 1990

- (i) SEQUENCE CHARACTERISTICS:
- 30 (A) LENGTH: 1377 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- 35 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Eremothecium gossypii*
- (C) ACCESSION NUMBER: A29820
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1990

	ATGGGTAAGG	AAAAGACTCA	CGTTAACGTT	GTCGTCATCG	GTCACGTCGA	50
	CTCTGGTAAG	TCTACTACCA	CCGGTCACTT	GATCTACAAG	TGTGGTGGTA	100
15	TTGACAAGAG	AACCATCGAG	AAGTTCGAGA	AGGAGGCTGC	CGAGTTGGGT	150
	AAGGGTTCTT	TCAAGTACGC	CTGGGTTTTG	GACAAATTGA	AGGCTGAGAG	200
	AGAGAGAGGT	ATCACCATCG	ACATTGCGTT	GTGGAAGTTC	GAGACTCCAA	250
	AGTACCACGT	CACTGTCATT	GACCCCCCAG	GCCACAGAGA	CTTCATCAAG	300
	AACATGATTA	CCGGTACTTC	TCAAGCTGAC	TGTGCCATCT	TGATCATTGC	350
50	TGGTGGTGTC	GGTGAGTTCG	AGGCTGGTAT	CTCCAAGGAC	GGTCAGACCA	400
	GAGAGCACGC	TTTGTTGGCT	TACACCTTGG	GTGTCAAGCA	GTTGATCGTT	450
	GCCATCAACA	AGATGGACTC	CGTCAAGTGG	GACGAGTCCA	GATACCAGGA	500
	GATTGTCAAG	GAGACCTCCA	ACTTCATCAA	GAAGGTCGGT	TACAACCCTA	550

	AGACTGTTCC	ATTTCGTTCCA	ATCTCCGGCT	GGAACGGTGA	CAACATGATT	600
	GAGGCCACCA	CCAACGCCCC	ATGGTACAAG	GGCTGGGAGA	AGGAGACCAA	650
	GGCTGGTGCC	GTCAAGGGTA	AGACCTTGTT	GGAGGCCATT	GACGCCATTG	700
	AGCCACCTGT	CAGACCAACT	GACAAGGCAT	TGAGATTGCC	ATTGCAGGAT	750
5	GTCTACAAGA	TCGGTGGTAT	TGGTACGGTT	CCAGTCGGCA	GAGTCGAGAC	800
	CGGTGTCATC	AAGCCAGGTA	TGGTTGTTAC	CTTCGCCCCA	TCCGGTGTCA	850
	CCACTGAAGT	CAAGTCCGTC	GAGATGCACC	ACGAGCAATT	GGAGGAGGGT	900
	GTCCCAGGTG	ACAACGTTGG	TTTCAACGTC	AAGAACGTCT	CCGTCAAGGA	950
	GATCAGAAGA	GGTAACGTTT	GCGGTGACTC	CAAGAACGAC	CCACCAAAGG	1000
10	CTGCTGAGTC	CTTCAACGCT	ACCGTCATTG	TCTTGAACCA	CCCAGGTCAA	1050
	ATCTCTGCCG	GTTACTCTCC	AGTCTTGAC	TGTCACACTG	CCCACATTGC	1100
	TTGTAAGTTC	GACGAGTTGT	TGGAGAAGAA	CGACAGAAGA	ACCGGTAAGA	1150
	AGTTGGAAGA	CTCTCCAAAG	TTCCTAAAGG	CCGGTGACGC	TGCCATGGTC	1200
	AAGTTTGTCC	CATCCAAGCC	AATGTGTGTT	GAGGCTTTCA	CCGACTACCC	1250
15	ACCATTGGGT	AGATTGCTG	TCAGAGACAT	GAGACAGACC	GTTGCTGTCTG	1300
	GTGTCATCAA	GTCTGTTGTC	AAGTCCGACA	AGGCTGGTAA	GGTCACCAAG	1350
	GCCGCCAAA	AGGCTGGTAA	GAAATAG			1377

20

## 2) INFORMATION FOR SEQ ID NO: 1991

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1646 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

30

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus oryzae*  
 (B) STRAIN: KBN616  
 (C) ACCESSION NUMBER: AB007770

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1991

	TGGGGTAAGT	TTATCAACCC	GTCGAGTTGT	GTTGCATCTC	AGATCATGGC	50
	TGACAAGTAC	TTTCCTCCTT	ACAGTAAGGA	AGACAAGCAG	CACATCAACA	100
40	TCGTGCTTAT	CGGCCACGTC	GATTCCGGCA	AGTCCACCAC	CACTGGTCAC	150
	TTGATCTACA	AGTGTGGTGG	TATCGACCAG	CGTACCATCG	AGAAGTTCGA	200
	GAAGGAAGCC	GCTGAGCTCG	GTAAGGGTTC	CTTCAAGTAC	GCCTGGGTTC	250
	TTGACAAGCT	CAAGTCCGAG	CGTGAGCGTG	GTATCACCAT	CGATATCGCC	300
	CTCTGGAAGT	TCCAGACCTC	CAAGTATGAG	GTCACCGTCA	TTGGTAAGCA	350
45	TTTGAGTTCC	AACCTACGTT	GCCCAACATT	TACAGTCATC	TAACAAAGTT	400
	CAATAGATGC	CCCCGGTCAC	CGTGACTTCA	TCAAGAACAT	GATCACTGGT	450
	ACTTCCAGG	CTGACTGCGC	TATCCTCATC	ATTGCCCTCCG	GTACTGGTGA	500
	ATTGAGGGCT	GGTATCTCCA	AGGATGGTCA	GACCCGTGAG	CACGCTCTGC	550
	TCGCTTTCAC	CCTCGGTGTC	CGTCAGCTCA	TCGTTGCCCT	CAACAAGATG	600
50	GACACCTGCA	AGTGGTCTCA	GGATCGTTAC	AACGAAATCG	TTAAGGAGAC	650
	TTCCAACCTC	ATCAAGAAGG	TCGGATACAA	CCCCAAGAGC	GTTCTTTTCG	700
	TCCCCATCTC	CGGTTTCAAC	GGTGACAACA	TGATTGAGGC	CTCCACCAAC	750
	TGCCCCCTGGT	ACAAGGGCTG	GGAGAAGGAG	ACCAAGGCTG	GCAAGTCCAC	800

	CGGTAAGACC	CTTCTCGAGG	CCATCGATGC	CATCGAGCCC	CCCGTCCGTC	850
	CCACCGACAA	GCCTCTCCGT	CTTCCCCTCC	AGGATGTCTA	CAAGATCTCT	900
	GGTATCGGTA	CTGTGCCCCG	CGGTCGTGTC	GAGACTGGTG	TCATCAAGCC	950
	TGGTATGGTC	GTTACTTTCG	CTCCTGCCAA	CGTGACCACT	GAAGTCAAGT	1000
5	CCGTTGAAAT	GCACCACCAG	CAGCTCCAGG	CCGGTAACCC	CGGTGACAAC	1050
	GTTGGTTTCA	ACGTCAAGAA	CGTCTCCGTC	AAGGAAGTCC	GCCGTGGTAA	1100
	CGTTGCCGGT	GACTCCAAGA	ACGACCCCCC	TGCTGGCTGC	GATTCCTTCA	1150
	ACGCCCAGGT	CATCGTCCTT	AACCACCCCG	GTCAGGTCGG	CAACGGTTAC	1200
	GCTCCCGTCC	TGGACTGCCA	CACCGCTCAC	ATTGCTTGCA	AGTTCGCTGA	1250
10	GCTCCTTGAG	AAGATTGACC	GCCGTACCGG	TAAATCTGTT	GAGGACAAGC	1300
	CCAAGTTCAT	CAAGTCTGGT	GATGCTGCCA	TCGTCAAGAT	GATTCCTTCC	1350
	AAGCCCATGT	GTGTGGAGTC	TTTCACTGAC	TTCCCCCCTC	TTGGTCGTTT	1400
	CGCTGTCCGT	GACGTAAGTT	TTTCCCTCTT	GACTATCTTC	ACAATTTTTTC	1450
	ACATATTTTC	ACGCCTCGTC	CCACTCTTTT	TCCTCCCTTC	CTCTTTGGTT	1500
15	CCCCTTTTTG	CCTGCAAGTT	CTCTATAGCT	AACATGATGT	CTAGATGCGT	1550
	CAAAGTGTG	CCGTCGGAGT	TATCAAGTCG	GTTGAGAAGA	ACACTGGCGG	1600
	TTCTGGCAAG	GTCACCAAGG	CCGCCAGAA	GGCTGGCAAG	AAATAA	1646

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## 2) INFORMATION FOR SEQ ID NO: 1992

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1380 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

30

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aureobasidium pullulans*
- (B) STRAIN: R106
- (C) ACCESSION NUMBER: U19723

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1992

	ATGGGTAAGG	AAAAGTCCCA	CATCAACGTC	GTCGTTATCG	GCCACGTCGA	50
	CTCCGGTAAG	TCGACCACCA	CCGGTCACTT	GATCTACAAG	TGCGGTGGTA	100
40	TCGACAAGCG	TACCATCGAG	AAGTTCGAGA	AGGAAGCCGC	CGAACTCGGC	150
	AAGGGTTTCT	TCAAGTACGC	CTGGGTCCTC	GACAAGCTGA	AGTCTGAGCG	200
	TGAGCGTGGT	ATCACTATCG	ATATCGCTCT	GTGGAAGTTC	GAGACCCCCA	250
	AGTACATGGT	CACCGTCATC	GATGCCCCCG	GTCACCGTGA	TTTCATCAAG	300
	AACATGATCA	CTGGTACCTC	CCAGGCTGAC	TGCGCCATTC	TCATCATTGC	350
45	CGCCGGTACT	GGTGAGTTCG	AGGCTGGTAT	CTCCAAGGAT	GGCCAGACTC	400
	GTGAGCACGC	CCTTCTCGCC	TACACCCTTG	GTGTCAAGCA	GCTCATCGTC	450
	GCTATCAACA	AGATGGACAC	CACCAAGTGG	TCTGAGGCC	GTTACCAGGA	500
	GATCATCAAG	GAGACCTCCG	GTTTCATCAA	GAAGGTCGGC	TACAACCCCA	550
	AGCACGTTCC	CTTTGTCCCC	ATCTCGGGTT	TCAACGGTGA	CAACATGATT	600
50	GAGGTTTCTT	CCAAGTCCCC	CTGGTACAAG	GGTTGGGAGA	AGGAGACCAA	650
	GGCCAAGGCC	ACTGGTAAGA	CTCTCCTCGA	GGCCATTGAC	GCCATCGACC	700
	CTCCTTCGCG	CCCCACCGAC	AAGCCCCCTC	GTCTTCCCCT	CCAGGATGTC	750
	TACAAGATCG	GTGGTATTGG	CACGGTGCCC	GTCGGCCGTG	TCGAGACCGG	800

	TACCATCAAG	GGTGGTATGG	TCGTCACCTT	CGCCCCCGCT	GGTGTACCA	850
	CTGAGGTCAA	GTCCGTCGAG	ATGCACCACG	AGCAGCTCTC	CGAGGGTCTC	900
	CCCGGTGACA	ACGTCGGCTT	CAACGTCAAG	AACGTCTCCG	TCAAGGAGAT	950
	CCGTCGTGGT	AACGTTGCCG	GTGACTCCAA	GAACGACCCC	CCCAAGGGTT	1000
5	GCGACTCCTT	CAACGCCCAG	GTCATCGTCC	TCAACCACCC	CGGTCAGGTC	1050
	GGTGCTGGTT	ACGCACCCGT	CCTCGATTGC	CACACTGCCC	ACATCGCCTG	1100
	CAAGTTCTCC	GAGCTTGTTG	AGAAGATTGA	CCGCCGTACC	GGCAAGTCCG	1150
	TTGAGGCCCG	CCCCAAGTTC	ATCAAGTCTG	GTGACGCCGC	CATCGTCAAG	1200
	ATGGTTCCCT	CCAAGCCTAT	GTGTGTTGAG	GCCTTCACTG	ACTACCCTCC	1250
10	TCTCGGTCGT	TTCGCCGTCC	GTGACATGAG	ACAGACCGTC	GCTGTCGGTG	1300
	TCATCAAGTC	CGTCGCCAAG	TCCGACAAGC	AGGGTGCCGG	TAAGGTTACC	1350
	AAGGCCGCTG	TCAAGGCTGG	CAAGAAGTAA			1380

15

2) INFORMATION FOR SEQ ID NO: 1993

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 1383 bases
20	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

	(A) ORGANISM: <i>Histoplasma capsulatum</i>
	(B) STRAIN: 186AS
	(C) ACCESSION NUMBER: U14100

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1993

	ATGGGTAAGG	AAGACAAGAC	TCACATTAAC	CTCGTCGTCA	TCGGCCACGT	50
	CGATTCCGGC	AAATCTACCA	CCACTGGTCA	TTTGATCTAC	AAATGCGGTG	100
35	GTATTGACAG	CCGTACCATT	GAGAAGTTCG	AAAAGGAAGC	CGAAGAGTTG	150
	GGCAAGAAAT	CCTTCAAATA	TGCGTGGGTC	CTTGACAAAC	TGAAGTCTGA	200
	GCGTGAGCGT	GGTATCACCA	TCGATATTGC	CCTCTGGAAA	TTGAGACTC	250
	CGAAGTACAG	TGTCACGTGC	ATTGATGCTC	CCGGCCATCG	TGACTTCATC	300
	AAGAACATGA	TCACTGGTAC	CTCCCAGGCT	GACTGCGCTA	TCCTCATCAT	350
40	TGCTGCCGGT	ACTGGTGAGT	TCGAGGCTGG	TATCTCCAAG	GATGGCCAGA	400
	CTCGTGAGCA	CGCTCTGCTT	GCTTTCACCC	TTGGTGTGAG	GCAACTCATC	450
	GTTGCCATCA	ACAAGATGGA	CACCACCAAG	TGGTCCGAGT	CCCGTTTCAA	500
	CGAAATCATC	AAGGAGGTTT	CCAACTTCAT	CAAGAAGGTC	GGATATAACC	550
	CCAAGGCTGT	TCCCTTCGTG	CCAATCTCTG	GTTTCGAGGG	TGACAACATG	600
45	ATTGAACCCT	CCCCCAACTG	CACATGGTAC	AAGGGCTGGA	ACAAGGAGAC	650
	TGCCTCTGGC	AAGTCTTCTG	GTAAAACCCT	TCTCGATGCC	ATTGACGCCA	700
	TTGAACCCCC	AACCCGTCCT	ACCGATAAGC	CCCTCCGTCT	TCCCCTCCAG	750
	GATGTGTACA	AAATCTCTGG	TATTGGCACT	GTTCCCGTCG	GACGTGTTGA	800
	GACTGGTGTC	ATCAAGCCCCG	GTATGGTCGT	GACTTTCGCT	CCCTCCAACG	850
50	TCACCACTGA	AGTCAAGTCC	GTCGAAATGC	ACCACCAACA	ACTCCAGGCT	900
	GGTTACCCTG	GCGACAACGT	CGGCTTCAAC	GTCAAGAACG	TTTCAGTCAA	950
	GGAAGTCCGC	CGTGGCAACG	TTGCTGGCGA	CTCCAAAAT	GATCCCCCTA	1000
	AGGGCTGCGA	ATCCTTCAAT	GCCCAGGTCA	TCGTCCTTAA	CCACCCCGGC	1050



CAGGTTGGCG CTGGTTATGC CCCAGTCCTC GACTGCCACA CTGCCCACAT 1100  
 TGCTTGCAAG TTCTCTGAGC TTATTGAGAA GATCGACCGC CGTACCGGAA 1150  
 AGTCTGTTGA GAACAACCCC AAGTTCATCA AGTCTGGTGA TGCTGCTATC 1200  
 GTCAAGATGG TTCCCTCCAA GCCCATGTGC GTGGAGCCCT TCACTGACTA 1250  
 5 TCCCCCTCTT GGACGTTTCG CTGTCCGTGA CATGAGACAA ACCGTCGCTG 1300  
 TCGGTGTCAT CAAGTCCGTC ATCAAGTCTG ACAAGACTGC TGGCAAGGTC 1350  
 ACCAAGGCCG CGCAGAAGGC CACCAAGAAA TAA 1383

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## 2) INFORMATION FOR SEQ ID NO: 1994

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1383 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Neurospora crassa*  
 (C) ACCESSION NUMBER: D45837

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1994

ATGGGCAAGG AGGACAAGAC TCACATCAAC GTCGTCGTTA TCGGCCACGT 50  
 CGATTCCGGC AAGTCTACCA CTACCGGTCA CTTGATCTAC AAGTGCGGTG 100  
 GTATCGACAA GCGTACCATC GAGAAGTTCG AGAAGGAAGC CGCTGAGCTC 150  
 30 GGTAAGGGTT CCTTCAAGTA TGCCTGGGTT CTTGACAAGC TCAAGGCCGA 200  
 GCGTGAGCGT GGTATCACCA TCGATATCGC CCTCTGGAAG TTCGAGACTC 250  
 CCAAGTACTA CGTCACCGTC ATCGATGCCC CCGGTCATCG TGATTTTCATC 300  
 AAGAACATGA TCACTGGTAC CTCCCAGGCT GATTGCGCTA TCCTCATCAT 350  
 TGCCGCCGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG GATGGCCAGA 400  
 35 CCCGTGAGCA CGCCCTGCTC GCCTACACCC TCGGTGTCAA GCAGCTCATT 450  
 GTTGCCATCA ACAAGATGGA CACCACCCAG TGGTCCCAGA CTCGTTTCGA 500  
 GGAGATCATC AAGGAGACCA AGAACTTCAT CAAGAAGGTT GGCTACAACC 550  
 CCGCTGGTGT CGCTTTCGTC CCCATCTCCG GCTTCAACGG CGACAACATG 600  
 CTTGAGCCCT CCACCAACTG CCCCTGGTAC AAGGGTTGGG AGAAGGAGAC 650  
 40 CAAGGCCGGC AAGGCCACTG GCAAGACCCT CCTCGAGGCC ATCGACGCCA 700  
 TTGAGCCCCC CAAGCGTCCT ACCGACAAGC CCCTCCGTCT TCCCCTCCAG 750  
 GATGTCTACA AGATCGGTGG TATCGGCACA GTGCCCGTCG GCCGTATCGA 800  
 GACTGGTGTC CTCAAGCCCG GTATGGTCGT TACCTTCGCT CCTTCCAACG 850  
 TCACCACTGA AGTCAAGTCC GTCGAGATGC ACCACGAGCA GCTTGCTCAG 900  
 15 GGTGTCCCCG GTGACAACGT CGGCTTCAAC GTGAAGAAGC TTTCCGTCAA 950  
 GGATATCCGC CGTGGTAACG TTGCCGGTGA CTCCAAGAAC GACCCCCCTG 1000  
 CTGGCGCCGC CTCTTTCACC GCCCAGGTCA TCGTTCTCAA CCACCCCGGT 1050  
 CAGGTCGGTG CCCGCTACGC CCCCCTCCTC GACTGCCACA CTGCCCACAT 1100  
 TGCCTGCAAG TTCGCCGAGC TCCTCGAGAA GATCGACCGC CGTACTGGTA 1150  
 50 AGGCTGTTGA GGCCTCCCCC AAGTTCATCA AGTCTGGTGA TGCTGCCATC 1200  
 GTCAAGATGA TTCCCTCCAA GCCCATGTGC GTTGAGGCTT TCACCGACTA 1250  
 CCCTCCCTC GGCCTTTTCG CCGTCCGTGA CATGCGTCAG ACCGTCGCCG 1300  
 TCGGTGTCAT CAAGGCCGTC GACAAGTCCA CCGTGCCGC TGGCAAGGTC 1350

ACCAAGTCCG CTGCCAAGGC CGCCAAGAAG TAA

1383

## 5 2) INFORMATION FOR SEQ ID NO: 1995

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1383 bases  
 (B) TYPE: Nucleic acid  
 10 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Podospira anserina*  
 (C) ACCESSION NUMBER: X74799

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1995

20 ATGGGCAAGG AGGACAAGAC TCACATCAAC GTCGTCGTTA TCGGCCACGT 50  
 CGATTCCGGC AAGTCGACCA CCACTGGTCA CTTGATCTAC AAGTGCGGTG 100  
 GTATTGACAA GCGTACCATC GAGAAGTTCG AGAAGGAAGC TGCTGAGCTC 150  
 GGCAAGGGCT CTTTCAAGTA TGCCTGGGTT CTTGACAAGT TGAAGGCCGA 200  
 25 GCGTGAGCGT GGTATCACCA TCGATATTGC CCTCTGGAAG TTCGAGACCC 250  
 CCAAGTACTA TGTCACCGTC ATTGATGCCC CCGGCCATCG TGATTTTCATC 300  
 AAGAACATGA TTAAGGTGAC TTCCAGGCC GATTGCGCCA TTCTCATCAT 350  
 TGCCGCCGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG GATGGCCAGA 400  
 CCCGTGAGCA CGCTCTCCTC GCCTACACCC TCGGTGTGAA GCAGCTCATC 450  
 30 GTCGCCATCA ACAAGATGGA CACCACCAAG TGGTCCGAGG CCCGCTTCAA 500  
 CGAGATCATC AAGGAGACCT CCAACTTCAT CAAGAAGGTC GGCTACAACC 550  
 CCAAGACTGT TGCCTTCGTC CCCATCTCCG GTTTCAACGG CGACAACATG 600  
 CTTGAGGCTT CCACCAACTG CCCCTGGTAC AAGGGCTGGG AGAAGGAGGT 650  
 CAAGGGTGGC AAGGCCACCG GCAAGACCCT CCTTGAGGCC ATCGACTCCA 700  
 35 TCGAGCCCCC CAAGCGTCCC ACCGACAAGC CCCTCCGTCT TCCCCCTCCAG 750  
 GATGTCTACA AGATCGGCGG TATCGGCACA GTCCCTGTCG GCCGTATCGA 800  
 GACTGGTATC CTCAAGCCCG GTATGGTCGT TACCTTCGCT CCTTCCAACG 850  
 TCACCACTGA AGTCAAGTCC GTCGAGATGC ACCACGAGCA GCTCGCTGAG 900  
 GGTGTTCCCG GTGACAACGT TGGTTTCAAC GTGAAGAACG TCTCCGTCAA 950  
 40 GGAAATCCGC CGTGGCAACG TTGCCGGTGA CTCCAAGAAC GACCCCCCCA 1000  
 TGGGCGCCGC CTCTTTTCGAT GCCCAGGTCA TCGTCCTCAA CCACCCCGGC 1050  
 CAGGTCGGTG CTGGTTACGC CCCCGTCTC GATTGCCACA CTGCCACAT 1100  
 CGCCTGCAAG TTCTCTGAGC TCCTGCAGAA GATCGACCGC CGTACTGGTA 1150  
 AGGCCGTTGA GGAGAGCCCC AAGTTCATCA AGTCTGGTGA TGCTGCCATC 1200  
 45 GTCAAGATGG TTCCCTCCAA GCCCATGTGC GTTGAGGCTT TCACTGAGTA 1250  
 CCCTCCCCTC GGTCGTTTCG CCGTCCGTGA CATGCGTCAG ACCGTCGCTG 1300  
 TCGGTGTCAT CAAGAAGGTC GAGAAGGCCG CTGCTGGTTC CGGCAAGGTT 1350  
 ACCAAGTCCG CTGCCAAGGC TGGCAAGAAA TAA 1383

50

## 2) INFORMATION FOR SEQ ID NO: 1996

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1386 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Podospira curvicolla*  
 (B) STRAIN: VLV  
 (C) ACCESSION NUMBER: X96614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1996

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15 ATGGGCAAGG AGGACAAGAC TCACATCAAC GTCGTCGTTA TCGGCCACGT      50
   CGATTCCGGC AAGTCGACCA CCACTGGTCA CTTGATCTAC AAGTGCGGTG      100
   GTATTGACAA GCGTACCATC GAGAAGTTCG AGAAGGAAGC TGCTGAGCTC      150
   GGCAAGGGCT CTTTCAAGTA TGCCTGGGTT CTTGACAAGT TGAAGGCCGA      200
20 GCGTGAGCGT GGTATCACCA TTGATATCGC CCTCTGGAAG TTCGAGACCC      250
   CCAAGTACTA TGTCACCGTC ATCGATGCCC CCGGCCATCG TGATTTTCATC      300
   AAGAACATGA TTA CTGGTAC TTCCAGGCC GATTGCGCCA TTCTCATCAT      350
   TGCCGCCGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG GATGGCCAGA      400
   CCCGTGAGCA CGCTCTCCTC GCCTACACCC TCGGTGTGAA GCAGCTCATC      450
25 GTCGCCATCA ACAAGATGGA CACCACCAA TGGTCCGAGG CCCGCTTCAA      500
   CGAGATCATC AAGGAGACCT CCAACTTCAT CAAGAAGGTC GGCTACAACC      550
   CCAAGACTGT TGCCTTCGTC CCCATCTCCG GTTTCAACGG CGACAACATG      600
   CTTGAGGCTT CCACCAACTG CCCCTGGTAC AAGGGTTGGG AGAAGGAGGT      650
   CAAGGGTGGC AAGGCTACTG GCAAGACCCT CCTCGAGGCC ATCGACTCCA      700
30 TCGAGCCCCC CAAGCGTCCC ACCGACAAGC CCCTCCGTCT TCCCCTTCAG      750
   GACGTTTACA AGATCGGCGG TATCGGCACA GTCCCTGTCG GCCGTATCGA      800
   GACTGGTATC CTCAAGCCCG GTATGGTCGT TACCTTCGCC CCTTCCAACG      850
   TCACCACTGA AGTCAAGTCC GTCGAGATGC ACCACGAGCA GCTCTCTGAG      900
   GGTGTCCCCG GTGACAACGT TGGTTTCAAC GTGAAGAACG TCTCCGTCAA      950
35 GGAAATCCGC CGTGGCAACG TTGCCGGTGA CTCCAAGAAC GACCCCCCTC      1000
   TTGGCGCCGC TTCTTTTCGAT GCCCAGGTCA TCGTCCTCAA CCACCCCGGC      1050
   CAGGTCGGTG CTGGTTACGC CCCCCTCCTC GATTGCCACA CTGCCCACAT      1100
   CGCCTGCAAG TTCGCTGAGC TCCTGCAGAA GATCGATCGC CGTACTGGTA      1150
   AGGCTGTTGA GGAGAGCCCT AAGTTCATCA AGTCTGGTGA TGCTGCCATC      1200
40 GTCAAGATGA TTCCCTCCAA GCCCATGTGC GTTGAGGCTT TCACTGAGTA      1250
   CCCTCCCCTC GGTGCTTTCG CTGTCCGTGA CATGCGTCAG ACCGTCGCTG      1300
   TCGGTGTCAT CAAGAAGGTC GAGAAGGCCG CTGCTGGTTC CGGCAAGGTC      1350
   ACCAAGTCCG CTGCCAAGGC TGGTGGCAAG AAATAA      1386

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## 2) INFORMATION FOR SEQ ID NO: 1997

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1383 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Sordaria macrospora*  
 (B) STRAIN: 000  
 (C) ACCESSION NUMBER: X96615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1997

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10 ATGGGTAAGG AAGACAAGGC TCACATCAAC GTCGTCGTTA TCGGCCACGT      50
   CGATTCCGGC AAGTCCACCA CTACCGGTCA CCTGATCTAC AAGTGCGGTG      100
   GTATCGACAA GCGTACCATC GAGAAGTTCG AGAAGGAAGC CGCTGAGCTC      150
   GGCAAGGGTT CCTTCAAGTA TGCCTGGGTT CTTGACAAGC TCAAGGCCGA      200
15 GCGTGAGCGT GGTATCACCA TCGATATCGC CCTCTGGAAG TTCGAGACTC      250
   CCAAGTACTA CGTCACCGTC ATCGATGCCC CCGGCCATCG TGATTTTCATC      300
   AAGAACATGA TCACTGGTAC CTCCCAGGCT GATTGCGCTA TTCTCATCAT      350
   TGCCGCTGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG GATGGCCAGA      400
   CTCGTGAGCA CGCTCTTCTC GCCTACACCC TCGGTGTCAA GCAGCTCATC      450
20 GTTGCCATCA ACAAGATGGA CACCACCCAG TGGTCCCAGG CTCGTTTCGA      500
   GGAGATCATC AAGGAGACCA AGAACTTCAT CAAGAAGGTC GGCTACAACC      550
   CCGCCACCGT CGCTTTCGTC CCCATCTCCG GCTTCAACGG CGACAACATG      600
   CTTGAGGCCT CCACCAACTG CCCCTGGTAC AAGGGTTGGG AGAAGGAGAC      650
   CAAGGCCGGC AAGTCCACTG GCAAGACCCT CCTCGAGGCC ATCGACGCCA      700
25 TTGAGCAGCC CAAGCGCCCG ACCGACAAGC CCCTCCGTCT TCCCCTCCAG      750
   GATGTCTACA AGATCGGCGG TATCGGCACA GTGCCCGTCG GCCGTATCGA      800
   GACTGGTGTC CTCAAGCCCG GTATGGTCGT TACCTTCGCT CCTTCCAACG      850
   TCACCACTGA AGTCAAGTCC GTCGAGATGC ACCACGAGCA GCTTGCTCAG      900
   GGTGTTCCCG GTGACAACGT CGGCTTCAAC GTGAAGAACG TTTCCGTCAA      950
30 GGATATCCGT CGTGGTAACG TTGCCGGTGA CTCCAAGAAC GACCCCCCTG     1000
   TCGGCGCTGC CTCTTTCACC GCCCAGGTCA TCGTCCTTAA CCACCCCGGT     1050
   CAGGTCGGTG CCGGCTACGC TCCCGTCCTC GATTGCCACA CTGCCACAT      1100
   TGCCTGCAAG TTCGCCGAGC TCCTCGAGAA GATCGATCGC CGTACTGGTA      1150
   AGGCTGTTGA GACTTCTCCC AAGTTCATCA AGTCTGGTGA TGCTGCCATC      1200
35 GTCAAGATGA TTCCCTCCAA GCCCATGTGC GTCGAGGCTT TCACCGACTA      1250
   CCCTCCCCTC GGTCGTTTCG CCGTCCGTGA CATGCGTCAG ACCGTCGCTG      1300
   TCGGTGTCAT CAAGGCCGTC GACAAGACCC AGGCTGTCGC TGGCAAGGTC      1350
   ACCAAGTCTG CTGCCAAGGC TGCCAAGAAG TAA                          1383

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2) INFORMATION FOR SEQ ID NO: 1998

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1383 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichoderma reesei*

(B) STRAIN: QM9414  
(C) ACCESSION NUMBER: Z23012

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1998

5  
ATGGGTAAGG AGGACAAGAC TCACATCAAC GTGGTCGTCA TCGGCCACGT 50  
CGACTCCGGC AAGTCTACCA CCACTGGTCA CTTGATCTAC CAGTGCGGTG 100  
GTATCGACAA GCGTACCATT GAGAAGTTCG AGAAGGAAGC CGCCGAAGTC 150  
GGCAAGGGTT CCTTCAAGTA CGCGTGGGTT CTTGACAAGC TCAAGGCCGA 200  
10 GCGTGAGCGT GGTATCACCA TCGACATTGC CCTCTGGAAG TTCGAGACTC 250  
CCAAGTACTA TGTACCGTC ATTGACGCTC CCGGCCACCG TGACTTCATC 300  
AAGAACATGA TCACTGGTAC TTCCAGGCC GACTGCGCTA TCCTCATCAT 350  
CGCTGCCGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG GATGGCCAGA 400  
CCCGTGAGCA CGCTCTGCTC GCCTACACCC TGGGTGTCAA GCAGCTCATC 450  
15 GTCGCCATCA ACAAGATGGA CACTGCCAAC TGGGCCGAGG CTCGTTACCA 500  
GGAAATCATC AAGGAGACTT CCAACTTCAT CAAGAAGGTC GGCTTCAACC 550  
CCAAGGCCGT TGCTTTCGTC CCCATCTCCG GCTTCAACGG TGACAACATG 600  
CTCACCCCTT CCACCAACTG CCCCTGGTAC AAGGGCTGGG AGAAGGAGAC 650  
CAAGGCTGGC AAGTTCACCG GCAAGACCCT CCTTGAGGCC ATCGACTCCA 700  
20 TCGAGCCCCC CAAGCGTCCC ACGGACAAGC CCCTGCGTCT TCCCCTCCAG 750  
GACGTCTACA AGATCGGTGG TATCGGAACA GTTCCCGTCG GCCGTATCGA 800  
GACTGGTGTC CTCAAGCCCG GTATGGTCGT TACCTTCGCT CCCTCCAACG 850  
TCACCACTGA AGTCAAGTCC GTCGAGATGC ACCACGAGCA GCTCGCTGAG 900  
GGCCAGCCTG GTGACAACGT TGGTTTCAAC GTGAAGAAGC TTTCCGTCAA 950  
25 GGAAATCCGC CGTGGCAACG TTGCCGGTGA CTCCAAGAAC GACCCCCCCA 1000  
TGGGCGCCGC TTCTTTCACC GCCCAGGTCA TCGTCATGAA CCACCCCGGC 1050  
CAGGTCGGTG CCGGCTACGC CCCCGTCCCTC GACTGCCACA CTGCCCACAT 1100  
TGCCTGCAAG TTCGCCGAGC TCCTCGAGAA GATCGACCGC CGTACCGGTA 1150  
AGGCTACCGA GTCTGCCCCC AAGTTCATCA AGTCTGGTGA CTCCGCCATC 1200  
30 GTCAAGATGA TCCCCTCCAA GCCCATGTGC GTTGAGGCTT TCACCGACTA 1250  
CCCTCCCCTG GGTGTTTCG CCGTCCGTGA CATGCGCCAG ACCGTCGCTG 1300  
TCGGTGTGAT CAAGGCCGTC GAGAAGTCCT CTGCCGCCGC CGCCAAGGTC 1350  
ACCAAGTCCG CTGCCAAGGC CGCCAAGAAA TAA 1383

35

## 2) INFORMATION FOR SEQ ID NO: 1999

(i) SEQUENCE CHARACTERISTICS:  
40 (A) LENGTH: 29 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1999

CATGTCAAYA TTGGTACTAT TGGTCATGT  
50

29

## 2) INFORMATION FOR SEQ ID NO: 2000

1041

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 25 bases  
    (B) TYPE: Nucleic acid  
5      (C) STRANDEDNESS: Single  
    (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 10      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2000
- CCACCYTCIC TCAMGTTGAA RCGTT 25
- 15      2) INFORMATION FOR SEQ ID NO: 2001
- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 23 bases  
20      (B) TYPE: Nucleic acid  
    (C) STRANDEDNESS: Single  
    (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 25      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2001
- ACYACITTRA CIGCYGCIYAT YAC 23
- 30      2) INFORMATION FOR SEQ ID NO: 2002
- (i) SEQUENCE CHARACTERISTICS:  
35      (A) LENGTH: 21 bases  
    (B) TYPE: Nucleic acid  
    (C) STRANDEDNESS: Single  
    (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 40      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2002
- CCIGARGARA GAGCIMGWGG T 21
- 45      2) INFORMATION FOR SEQ ID NO: 2003
- 50      (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 21 bases  
    (B) TYPE: Nucleic acid  
    (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2003

CATYTCRAIR TTGTCACCTG G

21

## 2) INFORMATION FOR SEQ ID NO: 2004

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1360 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
- (B) STRAIN: SC5314
- (C) ACCESSION NUMBER: Genome project

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2004

GCTGCCTTCG	ACCGTTCTAA	ACCTCATGTC	AACATTGGTA	CTATTGGTCA	50
TGTTGATCAT	GGTAAACTA	CATTGACTGC	TGCTATCACC	AAAGTTTTAG	100
CCGAACAAGG	TGGTGCCAAC	TTCTTGGATT	ATGGTTCTAT	TGATAGAGCT	150
CCAGAAGAAA	GAGCTAGAGG	TATCACTATT	TCCACTGCCC	ACGTTGAATA	200
CGAAACCAAG	AACAGACACT	ATGCCCACGT	TGATTGTCCA	GGACACGCTG	250
ATTATATCAA	AAATATGATT	ACTGGTGCCG	CTCAAATGGA	TGGTGCTATC	300
ATTGTTGTTG	CTGCCACTGA	TGGTCAAATG	CCTCAAACCA	GAGAACATTT	350
GTTATTGGCC	AGACAAGTTG	GTGTTCAAGA	CTTGTTGTG	TTTGTCACAA	400
AAGTCGATAC	TATTGATGAC	CCTGAAATGT	TGGAATTAGT	CGAAATGGAA	450
ATGAGAGAAT	TGTTATCCAC	CTACGGTTTT	GATGGTGACA	ACACTCCAGT	500
TATTATGGGA	TCTGCTTTAA	TGGCTTTGGA	AGACAAGAAA	CCAGAAATTG	550
GTAAGGAAGC	TATCTTGAAA	TTGTTAGATG	CTGTCGATGA	ACACATTCCA	600
ACTCCATCAA	GAGACTTGGA	ACAACCATTT	TTGTTACCAG	TTGAAGACGT	650
GTTCTCCATC	TCCGGTAGAG	GAAGTGTGT	CACTGGTAGA	GTTGAAAGAG	700
GTGTTTTGAA	GAAGGGTGAA	GAAATCGAAA	TTGTTGGTGG	TTTTGACAAA	750
CCTTACAAGA	CTACTGTTAC	CGGTATTGAA	ATGTTCAAAA	AAGAATTAGA	800
CTCTGCTATG	GCTGGTGACA	ACTGTGGTGT	TTTGTTAAGA	GGTGTTAAAA	850
GAGATGAAAT	CAAGAGAGGT	ATGGTTTTGG	CCAAACCAGG	TACTGCTACT	900
TCTCACAAGA	AGTTCTTGGC	TTCTTGTAT	ATTTTGACTT	CCGAAGAAGG	950
TGGTCGTTCC	ACTCCATTG	GTGAAGGTTA	CAAGCCTCAA	TGCTTCTTCA	1000
GAAC TAACGA	TGTCCTACC	ACATTTTCAT	TCCCAGAAGG	AGAAGGTGTT	1050
GATCATTCTC	AAATGATCAT	GCCAGGTGAC	AACATTGAAA	TGCTTGGTGA	1100
ATTGATCAAA	TCTTGTCAT	TAGAAGTCAA	CCAACGTTTC	AACTTGAGAG	1150
AAGGTGGTAA	AACTGTTGGT	ACTGGTTTGA	TTACCAGAAT	CATCGAATAA	1200
ACAGAATGTG	CACTGTGAAT	AATAAAAAGA	AAAGAGGTAT	ATATAGGTGA	1250
CTTTGTATTT	TGTATTGAAC	AATAAAATTC	TGTAAATAGT	AAGGGCCTCA	1300
GAAGTTTTGA	TTTGATTTAT	GCCATGTGGA	CTTG TAGAGA	TATCCTTCTC	1350
AAACTTCTTG					1360

## 2) INFORMATION FOR SEQ ID NO: 2005

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1342 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double



(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Schizosaccharomyces pombe*

(C) ACCESSION NUMBER: Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2005

AAGCCGCATG	TCAATATTGG	TACTATTGGT	CATGTTGACC	ACGGTAAAAC	50
GACGTTGACG	GCTGCTATTA	CTAAATGCCT	TTCTGATCTT	GGTCAAGCTA	100
GTTTTATGGA	TTATAGTCAA	ATTGACAAGG	CCCCCGAGGA	AAAGGCACGT	150
GGTATTACCA	TTTCATCTGC	CCATGTTGAA	TACGAAACTG	CTAATCGTCA	200
CTATGCCCAT	GTGGATTGTC	CTGGTCACGC	CGATTACATT	AAGAATATGA	250
TTACTGGTGC	TGCTACAATG	GATGGCGCTA	TCATTGTTGT	TTCTGCTACC	300
GATGGTCAAA	TGCCTCAAAC	TCGTGAACAT	TTGCTTCTGG	CTCGTCAAGT	350
CGGTGTAAAG	CAAATTGTTG	TATACATCAA	TAAAGTCGAT	ATGGTCGAGC	400
CTGATATGAT	CGAGCTTGTC	GAAATGGAAA	TGCGTGAGCT	ACTCTCCGAA	450
TACGGATTTG	ATGGTGACAA	TACTCCAATT	GTTAGCGGCA	GTGCTTTATG	500
TGCCTTAGAG	GGTCGTGAGC	CTGAGATTGG	TCTCAATAGT	ATTACTAAAT	550
TGATGGAAGC	TGTTGATAGT	TATATTACTC	TTCTGAAAG	AAAAACGGAT	600
GTCCCTTTCT	TGATGGCCAT	CGAGGACGTT	TTTTCAATTT	CAGGTCGCGG	650
AACTGTAGTC	ACTGGCCGTG	TCGAGCGCGG	TACTTTAAAG	AAGGGTGCTG	700
AAATCGAAAT	CGTCGGTTAT	GGTAGCCATT	TAAAGACTAC	CGTTACTGGA	750
ATTGAAATGT	TCAAAAAGCA	GCTTGATGCC	GCCGTTGCCG	GTGACAATTG	800
TGGCCTTTTA	CTTCGTTCTA	TCAAGCGAGA	GCAATTAAAA	CGTGGAATGA	850
TTGTCGCTCA	ACCAGGAACC	GTTGCTCCTC	ATCAGAAATT	CAAGGCATCA	900
TTCTATATTT	TGACAAAAGA	GGAAGGAGGT	CGTCGTACCG	GTTTCGTTGA	950
CAAGTATCGT	CCCCAACTGT	ACAGTCGTAC	TTCCGACGTT	ACTGTCGAAC	1000
TTACCCACCC	TGATCCTAAC	GACTCAGACA	AAATGGTTAT	GCCTGGAGAC	1050
AATGTCGAGA	TGATCTGTAC	GCTTATTAC	CCCATTTGTCA	TCGAAAAAGG	1100
ACAACGCTTC	ACAGTTCGTG	AGGGTGGAAG	CACTGTAGGC	ACAGCTTTGG	1150
TTACTGAACT	TTTGGATTAG	TGCATTTATG	AACTTATTGG	CTTTAAAAAT	1200
TTTGCATGCT	GAATACCAAT	ATTATGTCCC	TTCTCAGAAT	TCTATAACTA	1250
CAGTGTCATT	ATTGTAATAA	GACTTTTGCA	TCCATTGACA	ATGGTATTTG	1300
ATACTTTTAT	AGTTTCTACT	ATTGTTAGCC	AAAGTTATAA	AA	1342

2) INFORMATION FOR SEQ ID NO: 2006

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2006

TGGAGCCGGT GAGCGTGG

18

2) INFORMATION FOR SEQ ID NO: 2007

1045

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2007

TGGAGCCAGT GAGCGTGG

18

2) INFORMATION FOR SEQ ID NO: 2008

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2008

TCTGGAGCCG ATGAGCGTG

19

2) INFORMATION FOR SEQ ID NO: 2009

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2009

CTGGAGCCAG TAAGCGTGG

19

2) INFORMATION FOR SEQ ID NO: 2010

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 861 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*  
 (B) STRAIN: KMK107  
 (C) ACCESSION NUMBER: AF027199

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2010

```

ATGAGTATTC AACATTTTTCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT      50
TTGCCTTCCT GTTTTGTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG      100
CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAACT GGATCTCAAC      150
AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT      200
GAGCACTTTT AAAGTTCTGC TATGTGGTGC GGTATTATCC CGTGTTGACG      250
CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG      300
GTTAAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT      350
AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCTGCCA      400
ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTTG      450
CACAACTGG GGGATCATGT AACTCGCCTT GATCGTTGGG AACC GGAGCT      500
GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGACG CCTGCAGCAA      550
TGGCAACAAC GTTGCGCAAA CTATTAAGTG GCGAACTACT TACTCTAGCT      600
TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC      650
ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG      700
GAGCCAGTGA GCGTGCGTCT CGCGGTATCA TTGCAGCACT GGGGCCAGAT      750
GGTAAGCCCT CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC      800
TATGGATGAA CGAAATAGAC AGATCGCTGA GATAGGTGCC TCACTGATTA      850
AGCATTGGTA A                                     861

```

## 2) INFORMATION FOR SEQ ID NO: 2011

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*  
 (B) STRAIN: CLSiS L-491  
 (C) ACCESSION NUMBER:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2011

```

ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT      50
TTGCTTTCCT GTTTTGTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG      100
CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAGCT GGATCTCAAC      150
AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT      200
GAGCACTTTT AAAGTTCTGC TATGTGGTGC GGTATTATCC CGTGTTGACG      250
CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG      300
GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT      350
AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCGGCCA      400
ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTTG      450
CACAACTGG GGGATCATGT AACC CGCCTT GATCGTTGGG AACC GGAGCT      500
GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA      550
TGGCAACAAC GTTGCGCAAA CTATTAAGTG GCGAACTACT TACTCTAGCT      600

```

TCCCGGCAAC	AATTAATAGA	CTGGATGGAG	GCGGATAAAG	TTGCAGGACC	650
ACTTCTGCGC	TCGGCCCTTC	CGGCTGGCTG	GTTTATTGCT	GATAAATCTG	700
GAGCCAGTAA	GCGTGGATCT	CGCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ATGACGGGGA	GTCAGGCAAC	800
TATGGATGAA	CGAAATAGAC	AGATCGCTGA	GATAGGTGCC	TCACTGATTA	850
AGCATTGGTA	A				861

## 2) INFORMATION FOR SEQ ID NO: 2012

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2012

CCGCGGATTA TTAAACCGCC CTTCCGCGG-MR-HEG-ATGTCAGAGG GATAGATCCA 49

## 2) INFORMATION FOR SEQ ID NO: 2013

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera ascorbata*
- (B) STRAIN: ATCC 33433

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2013

AGCTTAAGAA	CTCTTATCTG	GATTACGCGA	TGTCGGTCAT	TGTTGGCCGT	50
GCGCTGCCCG	ATGTCCGAGA	TGGCCTGAAG	CCGGTACACC	GTCGCGTACT	100
TTACGCCATG	AACGTATTGG	GCAATGACTG	GAACAAAGCC	TACAAAAAAT	150
CAGCCCGTGT	CGTGGGTGAC	GTGATCGGTA	AATATCACCC	GCATGGTGAT	200
ACTGCCGTCT	ATGACACTAT	CGTCCGTATG	GCACAGCCAT	TCTCACTGCG	250
ATACATGCTG	GTAGATGGTC	AAGGTAACCT	CGGTTCTGTC	GATGGCGACT	300
CCGCCGCAGC	GATGCGTTAT	ACGGAAATCC	GTATGTCGAA	AATCGCCCAT	350
GAG					353

## 2) INFORMATION FOR SEQ ID NO: 2014

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera georgiana*
- (B) STRAIN: ATCC 51603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2014

AGCTCCTATC	TGGATTATGC	GATGTCGGTC	ATTGTTGGCC	GTGCGCTGCC	50
AGATGTCCGA	GATGGCCTGA	AGCCGGTACA	CCGTCGCGTA	CTTTACGCCA	100
TGAACGTACT	AGGCAATGAC	TGGAACAAAG	CCTATAAAAA	ATCTGCCCGT	150
GTCGTTGGTG	ACGTAATCGG	TAAATACCAT	CCCCATGGTG	ACTCGGCGGT	200
CTATGACACG	ATCGTCCGCA	TGGCGCAGCC	ATTCTCGCTG	CGTTATATGC	250
TGGTAGACGG	TCAGGGTAAC	TTCGGTTCTA	TCGACGGCGA	CTCTGCGGCG	300
GCAATGCGTT	ATACGGAAAT	CCGTCTGGCG	AAAATTGCCC	ATGAACTGAT	350
GGCCG					355

## 2) INFORMATION FOR SEQ ID NO: 2015

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2015

CCAAGAAGCT CAAAAACATC TG

22

## 2) INFORMATION FOR SEQ ID NO: 2016

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2016

TADCCTGTCC AWACAGCCAT

20

## 2) INFORMATION FOR SEQ ID NO: 2017

(i) SEQUENCE CHARACTERISTICS:

1049

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2017

ACTTTGAATA AGGTCGGTCT AG

22

2) INFORMATION FOR SEQ ID NO: 2018

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2018

ACACTAAACA AGGTTGGTTT AG

22

2) INFORMATION FOR SEQ ID NO: 2019

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2019

ACACTAAACA AGGTCGGTCT AG

22

2) INFORMATION FOR SEQ ID NO: 2020

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2020

GTAGCTCCAG ATGAAATGTT TG

22

## 2) INFORMATION FOR SEQ ID NO: 2021

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2021

GTAGCTCCAG ACGAAATGTT TG

22

## 2) INFORMATION FOR SEQ ID NO: 2022

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2022

GTAGCTCCAG ATGAAACGTT TG

22

## 2) INFORMATION FOR SEQ ID NO: 2023

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2023

GTAAGTCCAG ATGAAATGTT TG

22

## 2) INFORMATION FOR SEQ ID NO: 2024

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid

1051

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2024

AGTGAAAAGA TGGCTGCTGC

20

2) INFORMATION FOR SEQ ID NO: 2025

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2025

AGTGAGAAAA TGGCTGCTGC

20

2) INFORMATION FOR SEQ ID NO: 2026

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2026

TCCAAGCATG CATTATGCAA ACG

23

2) INFORMATION FOR SEQ ID NO: 2027

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2027

TCGGTCTAGA TAGAGCTAAA ACG

23



## 2) INFORMATION FOR SEQ ID NO: 2028

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2028

TATGCTCTTC AACATCACG

20

## 2) INFORMATION FOR SEQ ID NO: 2029

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2029

AGCCGTTGAG ACTTTGAATA AG

22

## 2) INFORMATION FOR SEQ ID NO: 2030

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2030

CTTAATGGTC TTGGTATCG

19

## 2) INFORMATION FOR SEQ ID NO: 2031

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1053

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2031

CGTGACTGGG GTTCTGCTAT GA

22

2) INFORMATION FOR SEQ ID NO:2032

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2032

CGTGACTGGG GATCATCAAT GA

22

2) INFORMATION FOR SEQ ID NO: 2033

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2033

CGTGACTGGG GTTCTGCCAT GA

22

2) INFORMATION FOR SEQ ID NO: 2034

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2034

ATCAAGAACA CTGGCTATGT AG

22

## 2) INFORMATION FOR SEQ ID NO: 2035

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2035

ATCAAGAACA CTGGCTACGT AG

22

## 2) INFORMATION FOR SEQ ID NO: 2036

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2036

ATCAAGAACA CTGGTTACGT AG

22

## 2) INFORMATION FOR SEQ ID NO: 2037

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2037

ATCAAAAATA CTGGTTATGT AG

22

## 2) INFORMATION FOR SEQ ID NO: 2038

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1055

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2038

ATCAAGAATA CTGGCTACGT AG

22

2) INFORMATION FOR SEQ ID NO: 2039

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2039

ATCAAAAACA CTGGCTATGT AG

22

2) INFORMATION FOR SEQ ID NO: 2040

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2040

TGTGACCCCA GACAAACCC

19

2) INFORMATION FOR SEQ ID NO: 2041

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2041

GTTGAGCGGC AGCACTATCT

20

2) INFORMATION FOR SEQ ID NO: 2042

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2042

CACGGGGATT TCTCTATTTA

20

2) INFORMATION FOR SEQ ID NO: 2043

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2043

CACGGGGATT ACTCTATTTA

20

2) INFORMATION FOR SEQ ID NO: 2044

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2044

ACCGTAAGTC GGCCAAGTCA

20

2) INFORMATION FOR SEQ ID NO: 2045

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2045

1057

GTTCTTTCTC CGTATCGTC

19

## 2) INFORMATION FOR SEQ ID NO: 2046

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2046

ACGGGGATTT TTCTATCTAT

20

## 2) INFORMATION FOR SEQ ID NO: 2047

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2160 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: CS109
- (C) ACCESSION NUMBER: Z49094

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2047

ATGAACAAAC	CAACGATTCT	GCGCCTAATC	AAGTATCTGA	GCATTAGCTT	50
CTTAAGCTTG	GTTATCGCAG	CCATTGTCTT	AGGCGGAGGA	GTTTTTTTCT	100
ACTATGTTAG	CAAGGCTCCT	AGCCTATCCG	AGAGTAAACT	AGTTGCAACA	150
ACCTCTAGTA	AAATCTACGA	CAATAAAAAT	CAACTCATTG	CTGACTTGGG	200
TTCTGAACGC	CGCGTCAATG	CCCAAGCTAA	TGATATTCCC	ACAGATTTGG	250
TTAAGGCAAT	CGTTTCTATC	GAAGACCATC	GCTTCTTCGA	CCACAGGGGG	300
ATTGATACCA	TCCGTATCCT	GGGAGCTTTC	TTGCGCAATC	TGCAAAGCAA	350
TTCCCTCCAA	GGTGGATCAA	CTCTCACCCA	ACAGTTGATT	AAATTGACTT	400
ACTTTTCAAC	CTCGACTTCC	GACCAGACTA	TTTCTCGTAA	GGCTCAGGAA	450
GCTTGGTTAG	CGATTCAAGT	AGAACA AAAA	GCAACCAAAC	AGGAAATCTT	500
GACCTACTAT	ATAAATAAGG	TCTACATGTC	TAATGGCAAC	TATGGAATGC	550
AGACAGCAGC	TCAAAACTAC	TATGGTAAAG	ACCTCAATAA	TTTAAGTTTA	600
CCTCAGTTAG	CCTTGCTGGC	TGGAATGCCT	CAGGCACCAA	ACCAATATGA	650
CCCCTATTCA	CATCCAGAAG	CAGCCCAAGA	CCGCCGAAAC	TTGGTCTTAT	700
CTGAAATGAA	AAATCAAGGT	TACATCTCTG	CTGAACAGTA	TGAGAAAGCA	750
GTCAATACAC	CAATTACTGA	TGGACTACAA	AGTCTCAAAT	CAGCAAGTAA	800
TTACCCTGCT	TACATGGATA	ATTACCTCAA	GGAAGTCATC	AATCAAGTTG	850
AAGAAGAAAC	TGGCTATAAC	CTTCTAACTA	CTGGGATGGA	TGTTTACACA	900

1058

AATGTAGACC	AAGAAGCTCA	AAAACATCTG	TGGGATATCT	ACAACTCCGA	950
TCAATACGTC	TCTTACCCTG	ACGATGATTT	GCAAGTCGCA	TCTACGGTCG	1000
TAGATGTTTC	AAATGGTAAA	GTCATCGCAC	AACTTGGTGC	TCGTCATCAA	1050
GCAAGTAATG	TTTCATTCGG	TACCAACCAG	GCCGTAGAAA	CCAATCGTGA	1100
CTGGGGATCA	TCAATGAAAC	CAATCACTGA	CTATGCTCCC	GCTTTAGAAT	1150
ATGGAGTCTA	TGACTCTACT	GCTTCTATTG	TACATGATGT	CCCTTATAAC	1200
TATCCTGGCA	CTGATACTCC	ACTCTACAAC	TGGGATCATG	TCTACTTTGG	1250
AAACATTACA	ATCCAGTATG	CTCTTCAACA	ATCACGAAAT	GTCACAGCCG	1300
TTGAGACTTT	GAATAAGGTC	GGTCTAGATA	GAGCTAAAAC	CTTCCTTAAT	1350
GGTCTTG GTA	TCGACTATCC	AAGCATGCAT	TATGCAAACG	CCATTTCAAG	1400
TAACACA A CT	GAATCCAACA	AAAAATATGG	TGCAAGTAGT	GAAAAAATGG	1450
CTGCTGCCTA	CGCTGCTTTT	GCTAATGGTG	GTATTTATCA	CAAACCAATG	1500
TATATCAATA	AAATCGTCTT	TAGTGATGGT	AGCGAAAAAG	AATTTTCTGA	1550
TGCTGGTACA	CGAGCTATGA	AAGAGACTAC	TGCCCTATATG	ATGACTGAAA	1600
TGATGAAAAC	TGTTTTAACT	TACGGAACAG	GACGTGGAGC	CTACCTACCA	1650
TGGCTTCCAC	AAGCAGGTAA	GACAGGTACT	TCTAACTATA	CTGACGAAGA	1700
AATTGAAAAG	TATATCAAGA	ACACTGGTTA	CGTAGCTCCA	GATGAAATGT	1750
TTGTAGGGTA	TACCCGTAAA	TATGCAATGG	CTGTTTGGAC	AGGATACTCA	1800
AATCGTCTAA	CTCCAATCAT	CGGAGATGGT	TTCTTTGTTG	CTGGTAAAGT	1850
CTATCGTTCA	ATGATAACTT	ACCTTTCTGA	AGATGACCAA	CCTGGAGATT	1900
GGACAATGCC	AGATGGCTTG	TATAGAAATG	GAGAATTCGT	ATTTAAAAAT	1950
GGTGCTCGTT	CTACGTGGAG	CTCACCTGCT	CCACAACAAC	CCCCATCAAC	2000
TGAAAGTTCA	AGCTCATCAT	CAGATAGTTC	AACTTCACAG	TCTAACTCAA	2050
CCACTCCAAG	CACAAATAAT	AGTACGACTA	CCAATCCTAA	CAATAATACG	2100
CAACAATCAA	ATACAACCCC	TGATCAACAA	AATCAGAATC	CTCAACCAGC	2150
ACAACCATAA					2160

## 2) INFORMATION FOR SEQ ID NO: 2048

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2160 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: R6
- (C) ACCESSION NUMBER: M90527

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2048

ATGAACAAAC	CAACGATTCT	GCGCCTAATC	AAGTATCTGA	GCATTAGCTT	50
CTTAAGCTTG	GTTATCGCAG	CCATTGTCTT	AGGCGGAGGA	GTTTTTTTCT	100
ACTACGTTAG	CAAGGCTCCT	AGCCTATCCG	AGAGTAAACT	AGTTGCAACA	150
ACTTCTAGTA	AAATCTACGA	CAATAAAAAT	CAACTCATTG	CTGACTTGGG	200
TTCTGAACGC	CGCGTCAATG	CCCAAGCTAA	TGATATTCCC	ACAGATTTGG	250
TTAAGGCAAT	CGTTTCTATC	GAAGACCATC	GCTTCTTCGA	CCACAGGGGG	300
ATTGATACCA	TCCGTATCCT	GGGAGCTTTC	TTGCGCAATC	TGCAAAGCAA	350
TTCCCTCCAA	GGTGGATCAG	CTCTCACTCA	ACAGTTGATT	AAGTTGACTT	400
ACTTTTCAAC	TTCGACTTCC	GACCAGACTA	TTTCTCGTAA	GGCTCAGGAA	450
GCTTG GTTAG	CGATT CAGTT	AGAACA AAAA	GCAACCAAGC	AAGAAATCTT	500
GACCTACTAT	ATAAATAAGG	TCTACATGTC	TAA TGGAAC	TATGGAATGC	550

AGACAGCAGC	TCAAAACTAC	TATGGTAAAG	ACCTCAATAA	TTTAAGTTTA	600
CCTCAGTTAG	CCTTGCTGGC	TGGAATGCCT	CAGGCACCAA	ACCAATATGA	650
CCCCTATTCA	CATCCAGAAG	CAGCCCAAGA	CCGCCGAAAC	TTGGTCTTAT	700
CTGAAATGAA	AAATCAAGGC	TACATCTCTG	CTGAACAGTA	TGAGAAAGCA	750
GTCAATACAC	CAATTACTGA	TGGGCTACAA	AGTCTCAAAT	CAGCAAGTAA	800
TTACCCTGCT	TACATGGATA	ATTACCTCAA	GGAAGTCATC	AATCAAGTTG	850
AAGAAGAAAC	AGGCTATAAC	CTACTCACAA	CTGGGATGGA	TGTCTACACA	900
AATGTAGACC	AAGAAGCTCA	AAAACATCTG	TGGGATATTT	ACAATACAGA	950
CGAATACGTT	GCCTATCCAG	ACGATGAATT	GCAAGTCGCT	TCTACCATTG	1000
TTGATGTTTC	TAACGGTAAA	GTCATTGCCC	AGCTAGGAGC	ACGCCATCAG	1050
TCAAGTAATG	TTTCCTTCGG	AATTAACCAA	GCAGTAGAAA	CAAACCGCGA	1100
CTGGGGATCA	ACTATGAAAC	CGATCACAGA	CTATGCTCCT	GCCTTGGAGT	1150
ACGGTGTCTA	CGAGTCAACT	GCCACTATCG	TTCACGATGA	GCCCTATAAC	1200
TACCCTGGGA	CAAATACCCC	TGTTTATAAC	TGGGATAGGG	GCTACTTTGG	1250
CAACATCACC	TTGCAATACG	CCCTGCAACA	ATCGCGAAAC	GTCCAGCCG	1300
TGGAAACTCT	AAACAAGGTC	GGACTCAACC	GCGCCAAGAC	TTTCCTAAAT	1350
GGTCTCGGAA	TCGACTACCC	AAGTATTAC	TACTCAAATG	CCATTTCAAG	1400
TAACACAACC	GAATCAGACA	AAAAATATGG	AGCAAGTAGT	GAAAAGATGG	1450
CTGCTGCTTA	CGCTGCCTTT	GCAAATGGTG	GAAGTTACTA	TAAACCAATG	1500
TATATCCATA	AAGTCGTCTT	TAGTGATGGG	AGTGAAAAAG	AGTTCTCTAA	1550
TGTCGGAAC	CGTGCCATGA	AAGAAACGAC	AGCCTATATG	ATGACCGACA	1600
TGATGAAAAC	AGTCTTGAGT	TATGGAACTG	GACGAAATGC	CTATCTTGCT	1650
TGGCTCCCTC	AGGCTGGTAA	AACAGGAACC	TCTAACTATA	CAGACGAGGA	1700
AATTGAAAAC	CACATCAAGA	CCTCTCAATT	TGTAGCACCT	GATGAACAT	1750
TTGCTGGCTA	TACGCGTAAA	TATTCAATGG	CTGTATGGAC	AGGCTATTCT	1800
AACCGTCTGA	CACCACTTGT	AGGCAATGGC	CTTACGGTCG	CTGCCAAAGT	1850
TTACCGCTCT	ATGATGACCT	ACCTGTCTGA	AGGAAGCAAT	CCAGAGGATT	1900
GGAATATACC	AGAGGGGCTC	TACAGAAATG	GAGAATTCGT	ATTTAAAAAT	1950
GGTGCTCGTT	CTACGTGGAG	CTCACCTGCT	CCACAACAAC	CCCCATCAAC	2000
TGAAAGTTCA	AGCTCATCAT	CAGATAGTTC	AAGTTTACAG	TCTAGCTCAA	2050
CCACTCCAAG	CACAAATAAT	AGTACGACTA	CCAATCCTAA	CAATAATACG	2100
CAACAATCAA	ATACAACCCC	TGATCAACAA	AATCAGAATC	CTCAACCAGC	2150
ACAACCATAA					2160

## 2) INFORMATION FOR SEQ ID NO: 2049

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2160 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: URU-E159
- (C) ACCESSION NUMBER: AF139890

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2049

ATGAACAAAC	CAACGATTCT	GCGCCTAATC	AAGTATCTGA	GCATTAGCTT	50
CTTAAGCTTG	GTTATCGCAG	CCATTGTCTT	AGGCGGAGGA	GTTTTTTTCT	100
ACTACGTTAG	CAAGGCTCCT	AGCCTATCCG	AGAGTAAACT	AGTTGCAACA	150
ACTTCTAGTA	AAATCTACGA	CAATAAAAAT	CAACTCATTG	CTGACTTGGG	200



TTCTGAACGC	CGCGTCAATG	CCCAAGCTAA	TGATATTCCC	ACAGATTTGG	250
TTAAGGCAAT	CGTTTCTATC	GAAGACCATC	GCTTCTTCGA	CCACAGGGGG	300
ATTGATTCCA	TCCGTATCCT	GGGAGCTTTC	TTGCGCAATC	TGCAAAGTAA	350
TTCCCTCCAA	GGTGGATCAA	CTCTCACCCA	ACAGTTGATT	AAGTTGACTT	400
ACTTTTCAAC	CTCGACTTCC	GACCAGACTA	TTTCTCGTAA	GGCTCAGGAA	450
GCTTGGTTAG	CGATTCAAGT	AGAACAAAAA	GCAACCAAAC	AGGAAATCTT	500
GACCTACTAT	ATAAATAAGG	TCTACATGTC	TAATGGCAAC	TATGGAATGC	550
AGACAGCAGC	TCAAAACTAC	TATGGTAAAG	ACCTCAATAA	TTTAAGTTTA	600
CCTCAGTTAG	CCTTGCTGGC	TGGAATGCCT	CAGGCACCAA	ACCAATATGA	650
CCCCTATTCA	CATCCAGAAG	CAGCCCAAGA	CCGCCGAAAC	TTGGTCTTAT	700
CTGAAATGAA	AAATCAAGGT	TACATCTCTG	CTGAACAGTA	TGAGAAAGCA	750
GTCAATACAC	CAATTACTGA	TGGACTACAA	AGTCTCAAAT	CAGCAAGTAA	800
TTACCCTGCT	TACATGGATA	ATTACCTCAA	GGAGGTCATC	AATCAAGTAG	850
AACAAGAAAC	TGGCTATAAC	CTTCTAACTA	CTGGGATGGA	TGTTTACACA	900
AATGTAGACC	AAGAAGCTCA	AAAACATCTG	TGGGATATCT	ACAACTCCGA	950
TCAATACGTC	TCTTACCCTG	ACGATGATTT	GCAAGTCGCA	TCTACGGTCG	1000
TAGATGTTTC	AAATGGTAAA	GTCATCGCCC	AACTTGGAGC	TCGTCACCAA	1050
GCAAGTAAAC	TTTCATTGCG	TACCAACCAA	GCTGTGGAAA	CCAATCGTGA	1100
CTGGGGTTCT	GCTATGAAAC	CAATCACCGA	TTATGCACCT	GCCATAGAAT	1150
ACGGTGTGTTA	TGATTCCACT	GCAACTATGG	TTAATGATAT	TCCTTATAAC	1200
TATCCGGGAA	CAAGCACACC	TGTCTACAAC	TGGGATAGAG	CATATTTTCGG	1250
TAATATTACT	CTGCAATATG	CTCTTCAACA	ATCACGAAAT	GTCACAGCCG	1300
TTGAGACTTT	GAATAAGGTC	GGTCTAGATA	GAGCTAAAAC	CTTCCTTAAT	1350
GGTCTTGCTA	TCGACTATCC	AAGCATGCAT	TATGCAAACG	CCATTTCAAG	1400
TAATACAACA	GAATCTAATA	AACAATACGG	AGCAAGTAGT	GAAAAAATGG	1450
CTGCTGCTTA	TGCTGCCTTT	GCAAATGGTG	GCACTTACTA	TAAACCAATG	1500
TATATCCATA	AAGTCGTCTT	CAGTGATGGA	AGTAAAAAAG	AGTTCTCTAA	1550
TGTCGGAACT	CGTGCCATGA	AGGAAACGAC	AGCCTATATG	ATGACCGACA	1600
TGATGAAAAC	AGTCTTGACT	TATGGAAC TG	GGCGTGGAGC	CTATCTTCCT	1650
TGGCTTCCTC	AAGCTGGTAA	AACAGGAACC	TCTAACTATA	CAGATGAGGA	1700
AGTTGAAAAC	CACATCAAGA	ACACTGGCTA	TGTAGCTCCA	GATGAAATGT	1750
TTGTTGGTTA	TACTCGTAAG	TATTCTATGG	CTGTATGGAC	AGGTTATTTCG	1800
AATCGTTTAA	CTCCTATCGT	TGGAGATGGT	TTCTAGTTTG	CAGCTAAAGT	1850
TTATCGCTCA	ATGATAACGT	ATCTATCAGA	AGATACTCAT	CCAGAAGACT	1900
GGACGATGCC	AGACGGACTT	TTCAGAAATG	GAGAATTTCGT	ATTTAAAAAT	1950
GGTGCTCGTT	CTACGTGGAA	CTCACCTGCT	CCACAACAAC	CCCCATCAAC	2000
TGAAAGTTCA	AGCTCATCAT	CAGATAGTTC	AACTTCACAG	TCTAGCTCAA	2050
CCACTCCAAG	CACAAATAAT	AGTACGACTA	CCAATCCTAA	CAATAATACG	2100
CAACAATCAA	ATACAACCCC	TGATCAACAA	AATCAGAATC	CTCAACCAGC	2150
ACAACCATAA					2160

## 2) INFORMATION FOR SEQ ID NO: 2050

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: 8303; 35193
- (C) ACCESSION NUMBER: AF046230

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2050

CTGTGGGATA	TCTACAACTC	CGATCAATAC	GTCTCTTACC	CTGACGATGA	50
TTTGCAAGTC	GCATCTACGG	TCGTAGATGT	TTCAAATGGT	AAAGTCATCG	100
CCCAACTTGG	AGCTCGTCAC	CAAGCAAGTA	ACGTTTCATT	TGGTACCAAC	150
CAAGCTGTGG	AAACCAATCG	TGACTGGGGT	TCTGCTATGA	AACCAATCAC	200
CGATTATGCA	CCTGCCATAG	AATACGGTGT	TTATGATTCC	ACTGCAACTA	250
TGGTTAATGA	TATTCCTTAT	AACTATCCGG	GAACAAGCAC	ACCTGTCTAC	300
AACTGGGATA	GAGCATATTT	CGGTAATATT	ACTCTGCAAT	ATGCTCTTCA	350
ACAATCACGA	AATGTCACAG	CCGTTGAGAC	TTTGAATAAG	GTCGGTCTAG	400
ATAGAGCTAA	AACCTTCCTT	AATGGTCTTG	GTATCGACTA	TCCAAGCATG	450
CATTATGCAA	ACGCCATTTT	AAGTAATACA	ACAGAATCTA	ATAAACAATA	500
CGGAGCAAGT	AGTGAAAAAA	TGGCTGCTGC	TTATGCTGCC	TTTGCAAATG	550
GTGGCACTTA	CTATAAACCA	ATGTATATCC	ATAAAGTCGT	CTTCAGTGAT	600
GGAAGTAAAA	AAGAGTTCTC	TAATGTCGGA	ACTCGTGCCA	TGAAGGAAAC	650
GACAGCCTAT	ATGATGACCG	ACATGATGAA	AACAGTCTTG	ACTTATGGAA	700
CTGGGCGTGG	AGCCTATCTT	CCTTGGCTTC	CTCAAGCTGG	TAAAACAGGA	750
ACCTCTAACT	ATACAGATGA	GGAAGTTGAA	AACCACATCA	AGAACACTGG	800
CTATGTAGCT	CCAGATGAAA	TGTTTGTGG	TTATACTCGT	AAGTATTCTA	850
TGGCTGTATG	GACAGGTTAT	TCAATCGTT	TAACCTCCTAT	CGTTGGAGAT	900
GGTTTCCTAG	TTGCAGCTAA	AGTTTATCGC			930

## 2) INFORMATION FOR SEQ ID NO: 2051

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: 63509; M11
- (C) ACCESSION NUMBER: AF046238

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2051

CTGTGGGATA	TTTACAATAC	AGACGAATAC	GTTGCCTATC	CAGATGATGA	50
CATGCAAGTA	GCTTCGACTA	TTGTAGATGT	ATCTAATGGT	AACGTTATTG	100
CACAACTTGG	TGCTCGTCAT	CAAGCAAGTA	ATGTTTCATT	CGGCACCAAC	150
CAGGCTGTGG	AGACCAATCG	TGACTGGGGT	TCTTCTATGA	AACCAATCAC	200
TGACTATGCT	CCCGCTTTAG	AATATGGAGT	CTATGACTCT	ACTGCTTCTA	250
TTGTACATGA	TGTTCTTAT	AACTATCCTG	GCACTGATAC	TCCAGTCTAC	300
AACTGGGATC	ATGTCTACTT	TGGAAACATT	ACAATCCAGT	ATGCTCTTCA	350
ACAATCACGA	AATGTCACAG	CCGTTGAGAC	TTTGAATAAG	GTCGGTCTAG	400
ATAGAGCTAA	AACCTTCCTT	AATGGTCTTG	GTATCGACTA	TCCAAGCATG	450
CATTATGCAA	ACGCCATTTT	AAGTAACACA	ACTGAATCCA	ACAAACAGTA	500
CGGTGCAAGT	AGTGAAAAGA	TGGCTGCTGC	TTATGCCGCC	TTTTCTAATG	550
GTGGTATTTA	CCACAAACCA	ATGTATATCA	ATAAAATCGT	CTTCAGTGAT	600
GGTAGTGAAA	AAGAATTTTC	TGATGCTGGT	ACACGAGCTA	TGAAAGAAAC	650
TACTGCCTAT	ATGATGACCG	AAATGATGAA	AACGTTTTTA	GCTTACGGAA	700
CCGGACGTGG	TGCTTACCTA	CCATGGCTTC	CACAAGCAGG	TAAGACAGGT	750

ACTTCTAACT	ATACTGACGA	CGAAATTGAA	AAGTATATCA	AGAACACTGG	800
CTACGTAGCT	CCAGATGAAA	TGTTTGTGG	TTATACTCGT	AAGTATTCTA	850
TGGCTGTATG	GACTGGTTAC	TCAAATCGTT	TAACTCCAAT	CGTAGGAGAT	900
GGTTTCCTAG	TTGCTGCTAA	GGTTTATCGC			930

## 2) INFORMATION FOR SEQ ID NO: 2052

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1195 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: #22/HA5
- (C) ACCESSION NUMBER: AB006877

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2052

GTCTCTTACC	CTGACGATGA	TTTGCAAGTC	GCATCTACGG	TCGTAGATGT	50
TTCCAATGGT	AAAGTCATCG	CCCAACTTGG	AGCTCGTCAC	CAAGCAAGTA	100
ACGTTTCATT	TGGTACCAAC	CAAGCTGTGG	AAACCAATCG	TGACTGGGGT	150
TCAACAATGA	AACCAATCAC	CGATTATGCA	CCTGCCATAG	AATACGGTGT	200
ATATGATTCC	ACTGCAACTA	TGGTTAATGA	TATTCCTTAT	AACTATCCGG	250
GAACAAGCAC	ACCTGTCTAC	AACTGGGATC	GAGCATATTT	TGGTAATATT	300
ACTCTGCAAT	ATGCCCTTCA	ACAATCACGT	AATGTTACAG	CAGTTGAAAC	350
ATTAAACAAG	GTTGGTTTAG	ATCGAGCCAA	AACTTTCCTA	AATGGCTTAG	400
GTATCGATTA	CCCAAGCATA	CACTATGCTA	ACGCCATTTC	AAGTAATACA	450
ACAGAATCTA	ACAAACATTA	CGGTGCAAGT	AGTGAAAAAA	TGGCTGCTGC	500
TTATGCCGCC	TTTGCTAATG	GTGGTATTTA	CCACAAACCA	ATGTATATCA	550
ATAAAATCGT	CTTTAGTGAT	GGTAGTGAGA	AAGAATTTTC	TGATGCTGGT	600
ACACGAGCTA	TGAAAGAAAC	TACTGCCTAT	ATGATGACCG	AAATGATGAA	650
AACTGTTTTA	GCTTACGGAA	CCGGACGTGG	TGCTTACCTA	CCATGGCTTC	700
CACAAGCAGG	TAAGACAGGT	ACTTCTAACT	ATACTGATGA	CGAAATCGAA	750
AAACATATCA	AGAATACTGG	CTACGTAGCT	CCAGATGAAA	TGTTTGTAGG	800
CTATACTCGT	AAGTATTCTA	TGGCTGTATG	GACTGGTTAC	TCAAATCGTT	850
TAACTCCAAT	TGTTGGAGAT	GGTTTCCTAG	TTGCTGCTAA	GGTTTATCGC	900
TCAATGATAT	CGTATCTATC	AGAAGATGAC	CAACCTGGAG	ATTGGACGAT	950
GCCAGACGGC	CTGTTCCGAA	ATGGAGAATT	CGTATTTAAA	AATGGTGCTC	1000
GTTCTACGTG	GAACTCACCT	GCTCCACAAC	AACCCCATC	AACTGAAAGT	1050
TCAAGCTCAT	CATCAGATAG	TTCAACTTCA	CAGTCTAGCT	CAACCACTCC	1100
AAGCACAAAT	AATAGTACGA	CTACCAATCC	TAACAATAAT	ACGCAACAAT	1150
CAAATACAAC	CCCTGATCAA	CAAAATCAGA	ATCCTCAACC	AGCAC	1195

## 2) INFORMATION FOR SEQ ID NO: 2053

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: 17619

(C) ACCESSION NUMBER: AF046237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2053

CTGTGGGATA	TTTACAATAC	AGACGAATAC	GTTGCCTATC	CAGACGATGA	50
ATTGCAAGTC	GCTTCTACCA	TTGTTGATGT	TTCTAACGGT	AAAGTCATTG	100
CCCAGCTAGG	AGCACGCCAT	CAGTCAAGTA	ATGTTTCCTT	CGGAATTAAC	150
CAAGCAGTAG	AAACAAACCG	CGACTGGGGA	TCAACTATGA	AACCGATCAC	200
AGACTATGCT	CCTGCCTTGG	AGTACGGTGT	CTACGATTCA	ACTGCTACTA	250
TCGTTACGGA	TGAGCCCTAT	AACTACCCTG	GGACAAATAC	TCCTGTTTAT	300
AACTGGGATA	GGGGCTACTT	TGGCAACATC	ACCTTGCAAT	ACGCCCTGCA	350
ACAATCGCGA	AACGTCCCG	CCGTGGAAAC	TCTAAACAAG	GTCGGACTCA	400
ACCGCGCCAA	GACTTTCCTA	AATGGTCTCG	GAATCGACTA	CCCAAGTATT	450
CACTACTCAA	ATGCCATTTC	AAGTAACACA	ACCGAATCAG	ACAAAAAATA	500
TGGAGCAAGT	AGTGAAAAGA	TGGCTGCTGC	TTACGCTGCC	TTTGCAAATG	550
GTGGAACCTA	CTATAAACCA	ATGTATATCC	ATAAAGTCGT	CTTTAGTGAT	600
GGGAGTGAAA	AAGAGTTCTC	TAATGTGCGA	ACTCGTGCCA	TGAAGGAAAC	650
GACAGCCTAT	ATGATGACCG	AAATGATGAA	AACAGTCTTG	AGTTATGGAA	700
CTGGACGAAA	TGCCTATCTT	GCTTGGCTTC	CTCAAGCTGG	TAAAACAGGT	750
ACCTCTAACT	ATACAGATGA	AGAAATTGAA	AAACACATCA	AAAACACTGG	800
CTATGTAGCT	CCAGATGAAA	CGTTTGTGTT	TTATACTCGT	AAGTATTCTA	850
TGGCTGTATG	GACAGGTTAC	ACAAACCGTC	TCACACCAAT	TGTGGGGGAT	900
GGCTTCACAG	TTGCTGCCAA	AGTTTACCGC			930

## 2) INFORMATION FOR SEQ ID NO: 2054

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 306 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: R6

(C) ACCESSION NUMBER: Y07845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2054

CGTCGCATTC	TCTACGGAAT	GAATGAATTG	GGTGTGACCC	CAGACAAACC	50
CCATAAAAAA	TCTGCTCGTA	TTACAGGGGA	TGTCATGGGT	AAATACCACC	100
CACACGGGGA	TTCCTCTATT	TATGAAGCCA	TGGTCCGTAT	GGCTCAATGG	150
TGGAGCTACC	GTTACATGCT	TGTAGATGGT	CATGGGAATT	TTGGTTCCAT	200
GGATGGAGAT	AGTGCTGCCG	CTCAACGTTA	TACCGAGGCA	CGTATGAGCA	250
AGATTGCTCT	GGAAATGCTT	CGTGATATCA	ACAAAAATAC	AGTTGATTTC	300
GTTGAT					306

## 2) INFORMATION FOR SEQ ID NO: 2055

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2472 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: 7785
- (C) ACCESSION NUMBER: Z67739

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2055

ATGTCTAACA	TTCAAAACAT	GTCCCTGGAG	GACATCATGG	GAGAGCGCTT	50
TGGTCGCTAC	TCCAAGTACA	TTATTCAAGA	CCGGGCTTTG	CCAGATATTC	100
GTGATGGGTT	GAAGCCGGTT	CAGCGCCGTA	TTCTTTATTC	TATGAATAAG	150
GATAGCAATA	CTTTTGACAA	GAGCTACCGT	AAGTCGGCCA	AGTCAGTCGG	200
GAACATCATG	GGGAATTTCC	ACCCACACGG	GGATTCTTCT	ATCTATGATG	250
CCATGGTTTCG	TATGTCACAG	AACTGGAAAA	ATCGTGAGAT	TCTAGTTGAA	300
ATGCACGGTA	ATAACGGTTC	TATGGACGGA	GATCCTCCTG	CGGCTATGCG	350
TTATACTGAG	GCACGTTTGT	CTGAAATTGC	AGGCTACCTT	CTTCAGGATA	400
TCGAGAAAAA	GACAGTTCCT	TTTGCATGGA	ACTTTGACGA	TACGGAGAAA	450
GAACCAACGG	TCTTGCCAGC	AGCCTTTCCA	AACCTCTTGG	TCAATGGTTC	500
GACTGGGATT	TCGGCTGGTT	ATGCCACAGA	CATTCCTCCC	CATAATTTAG	550
CTGAGGTCAT	AGATGCTGCA	GTTTACATGA	TTGACCACCC	AACTGCAAAG	600
ATTGATAAAC	TCATGGAATT	CTTACCTGGA	CCAGACTTCC	CTACAGGGGC	650
TATTATTTCAG	GGTCGTGATG	AAATCAAGAA	AGCTTATGAG	ACTGGGAAAG	700
GGCGCGTGGT	TGTTCTGTTCC	AAGACTGAAA	TTGAAAAGCT	AAAAGGTGGT	750
AAGGAACAAA	TCGTTATTAC	TGAGATTCCCT	TATGAAATCA	ATAAGGCCAA	800
TCTAGTCAAG	AAAATCGATG	ATGTTTCGTGT	TAATAACAAG	GTAGCTGGGA	850
TTGCTGAGGT	TCGTGATGAG	TCTGACCGTG	ATGGTCTTCG	TATCGCTATC	900
GAACCTTAAGA	AAGACGCTAA	TACTGAGCTT	GTTCTCAACT	ACTTATTTAA	950
GTACACCGAC	CTACAAATCA	ACTACAACCT	TAATATGGTG	GCGATTGACA	1000
ATTTACACCC	TCGTGAGGTT	GGGATTGTTT	CAATCCTGTC	TAGCTACATC	1050
GCTCACCGTC	GAGAAGTGAT	TTTGGCGCGT	TCACGCTTTG	ACAAAGAAAA	1100
GGCTGAGAAA	CGTCTCCATA	TCGTGCAAGG	TTTGATTTCGT	GTGATTTTCA	1150
TTTTTGATGA	AGTCATTGCT	CTTATCCGTG	CTTCTGAGAA	TAAGGCGGAC	1200
GCCAAGGAAA	ACCTCAAAGT	TAGCTATGAT	TTTACGGAAG	AACAGGCTGA	1250
GGCTATCGTA	ACTTTGCAAC	TGTACCGTTT	GACCAATACC	GATGTGGTTG	1300
TCTTGACAGGA	AGAAGAAGCA	GAGCTTCGTG	AGAAGATTGC	TATGCTGGCG	1350
GCTATTATCG	GTGATGAAAG	GACTATGTAC	AATCTCATGA	AGAAAGAACT	1400
TCGTGAGGTC	AAGAAGAAAT	TTGCAACTCC	TCGTTTGAGT	TCTTTAGAAG	1450
AACTGCGGAA	AGCAATTGAG	ATTGATACAG	CTAGTCTTAT	CGCTGAGGAA	1500
GATACCTACG	TCAGCGTGAC	CAAGGCAGGT	TACATCAAGC	GTACCAGTCC	1550
ACGTTTCCTTT	TCGGCTTCCA	CCTTGGAAGA	AATTGGCAAG	CGTGATGATG	1600
ACCGTTTGAT	TTTTGTTCAA	TCTGCCAAGA	CAACCCAGCA	CCTCTTGATG	1650
TTCACAAGTC	TTGGAAATGT	CATCTACAGA	CCAATCCATG	AGTTGGCAGA	1700
TATTCGTTGG	AAGGACATCG	GAGAGCATCT	GAGCCAAACC	ATCACAAACT	1750
TTGAAACGAA	TGAAGAAATC	CTTTATGTGG	AAGTACTGGA	TCAGTTTGAC	1800
GATGCGACAA	CCTACTTTGC	AGTGACTCGC	CTTGGTCAA	TCAAACGGGT	1850

AGAGCGAAAA	GAATTCACCTC	CATGGCGGAC	CTATAGATCT	AAGTCTGTCA	1900
AGTATGCTAA	GCTCAAAGAC	GATACAGATC	AGATTGTAGC	AGTGGCTCCG	1950
ATTAAACTAG	ATGATGTTGT	CTTGGTTAGT	CAAAATGGTT	ATGCCCTGCG	2000
TTTCAATATC	GAAGAGGTTT	CGGTTGTCGG	TGCTAAGGCA	GCAGGTGTCA	2050
AGGCTATGAA	TTTGAAAGAA	GATGATGTCC	TCCAATCTGG	CTTTATCTGT	2100
AATACTTCGT	CCTTCTACCT	CTTGACCCAG	CGTGGAAGCT	TGAAACGTGT	2150
TTCTATTGAG	GAAATTCTAG	CAACCAGCCG	TGCCAAACGA	GGATTACAAG	2200
TCTTGCGTGA	GTTGAAAAAC	AAACCGCATC	GTGTCTTCTT	GGCAGGAGCA	2250
GTTGCAGAGC	AAGGATTTGT	TGGCGATTTT	TTCAGTACGG	AAGTGGATGT	2300
GAACGACCAA	ACTCTGCTTG	TCCAATCCAA	TAAAGGAACA	ATCTATGAAA	2350
GCCGATTGCA	AGACTTGAAC	TTGTCAGAAC	GCACTAGCAA	TGGAAGCTTC	2400
ATTTCTGACA	CGATTTTCAGA	TGAAGAAGTT	TTTGACGCTT	ATCTTCAGGA	2450
AGTAGTTACT	GAAGATAAAT	AA			2472

## 2) INFORMATION FOR SEQ ID NO: 2056

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-16

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2056

AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
TACCCTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTAG	ATGTTTCAAA	100
TGGTAAAGTC	ATTGCCCAAC	TTGGAGCTCG	TCACCAAGCA	AGTAACGTTT	150
CATTTGGCAC	CAACCAAGCT	GTGGAAACCA	ATCGTGACTG	GGGTTCAACA	200
ATGAAACCAA	TCACAGACTA	TGCTCCTGCC	TTGGAATACG	GTGTCTACGA	250
TTCAACTGCT	ACTATCGTTC	ACGATGAGCC	CTATAACTAT	CCTGGGACAG	300
ATACCCCTGT	CTATAACTGG	GATAGGGGCT	ACTTTGGCAA	TATCACCTTG	350
CAATACGCCC	TGCAACAATC	GCGAAACGTC	CCAGCCGTGG	AAACACTAAA	400
CAAGGTCGGG	CTCAACCGCG	CCAAGACTTT	TCTAAATGGT	CTCGGAATCG	450
ACTACCCAAG	TATTCACTAC	TCAAATGCCA	TTTCAAGTAA	CACAACCGAG	500
TCAGACAAAA	AATATGGAGC	AAGTAGTGAA	AAGATGGCTG	CTGCTTACGC	550
TGCCTTTGCA	AATGGTGGAA	CTTACTATAA	ACCAATGTAT	ATCCATAAAG	600
TCGTCTTTAG	TGATGGAAGT	GAAAAAGAGT	TCTCTAATGT	CGGAACTCGC	650
GCCATGAAAG	AAACGACTGC	TTACATGATG	ACAGAAATGA	TGAAAACAGT	700
CTTGACGTAC	GGAATTGGTC	GTGGTGCCTA	CCTGCCTTGG	CTTCCTCAAG	750
CTGGTAAAC	AGGTACTTCT	AACTATACTG	ACGAAGAAAT	TGAAAAGTAT	800
ATCAAGAACA	CTGGTTACGT	AACTCCAGAT	GAAATGTTTG	TAGGGTATAC	850
CCGTAAATAT	GCAATGGCTG	TATGGACAGG	CTATTCTAAC	CGTCTGACAC	900
CACTTGTAGG	CGATGGCCTT	ACGGTCGCTG	CCAAGGTTTA	CCGCTCTATG	950
ATGACCTACC	TGTCTGAAGG	AAGCAATCCA	GAGGATTGGA	ATATACCAGA	1000
GGGGCTCTAC	AGAAATGGAG	AATTCGTATT	TAAAAATGGT	GCTCGTTCTA	1050
CGTGGAGCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	AAGTTCAAGC	1100
TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AGCTCAACCA	CTCCAAGCAC	1150
AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
CAACCCCTGA	TC				1212

## 2) INFORMATION FOR SEQ ID NO: 2057

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1242 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-17

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2057

ATGTAGACCA	AGAAGCTCAA	AAACATCTGT	GGGATATTTA	CAATACAGAC	50
GAATACGTTG	CCTATCCAGA	CGATGAATTG	CAAGTCGCTT	CTACCATTGT	100
TGATGTTTCT	AACGGGAAAG	TTATTGCTCA	GTTAGGTTCT	CGTCACCAAT	150
CAAGCAATGT	TTCTTCGGA	ATCAACCAAG	CTGTTGAAAC	CAACCGTGAC	200
TGGGGTTCTG	CCATGAAGCC	AATCACAGAC	TATGCTCCTG	CCTTAGAGTA	250
TGACATCTAC	GACTCAACTG	CTTCGATTGT	ACATGATGTT	CCTTATAACT	300
ATCCAGGTAC	TGATACTCCC	CTCTACAACT	GGGATAAAGT	CTACTTTGGA	350
AATATTACAA	TCCAGTATGC	ACTTCAACAG	TCACGTAATG	TCACAGCCGT	400
TGAGACTTTG	AATAAGGTCG	GTCTAGATAG	AGCTAAAACC	TTTCTTAATG	450
GTCTTGGTAT	CGACTATCCA	AGCATGCATT	ATGCAAACGC	CATTTCAAGT	500
AATACGACTG	AGTCAAACAA	AAAGTACGGA	GCAAGTAGTG	AGAAAATGGC	550
TGCTGCTTAC	GCTGCTTTTG	CTAACGGTGG	TATCTACCAT	AAACCAATGT	600
ATATCAACAA	AATCGTCTTT	AGCGATGGTA	GCTCAAAAGA	ATACGCTGAT	650
CCTGGTACTC	GTGCCATGAA	AGAGACGACC	GCCTATATGA	TGACAGAAAT	700
GATGAAGACT	GTCTTGGCAT	ACGGAACGGG	TCGTGGTGCT	TATCTCCCTT	750
GGCTACCTCA	AGCTGGTAAG	ACTGGTACAT	CAAACATATAC	AGATGATGAA	800
ATTGAAAAC	ACATCAAAAA	TACTGGTTAT	GTAGCTCCAG	ACGAAATGTT	850
TGTTGGTTAT	ACTCGCAAAT	ATTCAATGGC	GGTATGGACA	GGTACTCAA	900
ACCGCCTGAC	TCCTATCGTT	GGTGATGGCT	TCTATGTTGC	AGCTAAGGTT	950
TACCGTTCAA	TGATGACTTA	TCTGTCTGAG	GATAACAACC	CTGGCGACTG	1000
GACTATGCCA	GAAGGTCTCT	ATCGAAGTGG	TGAGTTCGTC	TTTAAAAAAG	1050
GTGCTCGTTC	TGCATGGACT	GCTCCTGCTC	CGCAACAGGC	CCCAACACCA	1100
GAAAGTTCGA	GCTCGACATC	AGAAAGTTCA	ACTTCACAGT	CAAGCTCAAC	1150
TACTCCAAGC	ACGAATAATA	GTGCAAACAA	TAATACCAAT	AACCAGCAAC	1200
CAAATACAAC	GCCTGGTCAA	CAAAACCAGA	ACCAAAATCA	GA	1242

## 2) INFORMATION FOR SEQ ID NO: 2058

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1225 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*  
 (B) STRAIN: StrR-18

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2058

GAAGCTCAAA	AACATCTGTG	GGATATTTAC	AATACAGACG	AATACGTTGC	50
CTATCCAGAC	GATGAATTGC	AAGTCGCTTC	TACCATTGTT	GATGTTTCTA	100
ACGGGAAAAGT	TATTGCTCAG	TTAGGTTCTC	GTCACCAATC	AAGCAATGTT	150
TCCTTCGGAA	TCAACCAAGC	TGTTGAAACC	AACCGTGA	GGGGTTCTGC	200
CATGAAGCCA	ATCACAGACT	ATGCTCCTGC	CTTAGAGTAT	GACATCTACG	250
ACTCAACTGC	TTCGATTGTA	CATGATGTTT	CTTATAACTA	TCCAGGTACT	300
GATACTCCCC	TCTACAAC	GGATAAAGTC	TACTTTGGAA	ATATTACAAT	350
CCAGTATGCA	CTTCAACAGT	CACGTAATGT	CACAGCCGTT	GAGACTTTGA	400
ATAAGGTCGG	TCTAGATAGA	GCTAAAACCT	TTCTTAATGG	TCTTGGTATC	450
GACTATCCAA	GCATGCATTA	TGCAAACGCC	ATTTCAAGTA	ATACGACTGA	500
GTCAAACAAA	AAGTACGGAG	CAAGTAGTGA	GAAAATGGCT	GCTGCTTACG	550
CTGCTTTTGC	TAACGGTGGT	ATCTACCATA	AACCAATGTA	TATCAACAAA	600
ATCGTCTTTA	GCGATGGTAG	CTCAAAAGAA	TACGCTGATC	CTGGTACTCG	650
TGCCATGAAA	GAGACGACCG	CCTATATGAT	GACAGAAATG	ATGAAGACTG	700
TCTTGGCATA	CGGAACGGGT	CGTGGTGCTT	ATCTCCCTTG	GCTACCTCAA	750
GCTGGTAAGA	CTGGTACATC	AAACTATACA	GATGATGAAA	TTGAAAATA	800
CATCAAAAAT	ACTGGTTATG	TAGCTCCAGA	CGAAATGTTT	GTTGGTTATA	850
CTCGCAAATA	TTCAATGGCG	GTATGGACAG	GTTACTCAA	CCGCCTGACT	900
CCTATCGTTG	GTGATGGCTT	CTATGTTGCA	GCTAAGGTTT	ACCGTTCAAT	950
GATGACTTAT	CTGTCTGAGG	ATAACAACCC	TGGCGACTGG	ACTATGCCAG	1000
AAGGTCTCTA	TGCAAGTGGT	GAGTTCGTCT	TTAAAAAAGG	TGCTCGTTCT	1050
GCATGGACTG	CTCCTGCTCC	GCAACAGGCC	CCAACACCAG	AAAGTTCGAG	1100
CTCGACATCA	GAAAGTTCAA	CTTCACAGTC	AAGCTCAACT	ACTCCAAGCA	1150
CGAATAATAG	TGCAACAAT	AATACCAATA	ACCAGCAACC	AAATACAACG	1200
CCTGGTCAAC	AAAACCAGAA	CCAAA			1225

## 2) INFORMATION FOR SEQ ID NO: 2059

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*  
 (B) STRAIN: StrR-38

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2059

TGGCTACTTT	GGAAACATTA	CAGTCCAGTA	TGCTCTTCAA	CAATCACGAA	50
ATGTCACAGC	CGTTGAGACT	TTGAATAAGG	TGGTCTAGA	TAGAGCTAAA	100
ACCTTCCTCA	ATGGACTTGG	TATCGATTAT	CCAAGCATGC	TTTATGCAAA	150
CGCCATTTC	AGTAACACAA	CTGAATCCAA	CAAAAAGTAC	GGAGCAAGTA	200
GTGAAAAAAT	GGCCGCTGCC	TACGCAGCTT	TTGCTAATGG	TGGTACTTAC	250
CACAAACCAA	TGTATATCAA	TAAAATCGTC	TTTAGTGATG	GTAGTGAAAA	300
AGAATTTTCT	GATGCCGGTA	CTCGGGCTAT	GAAAGAAACT	ACTGCCTATA	350



TGATGACCGA	AATGATGAAA	ACTGTCTTAT	TATACGGAAC	CGGACGTGGA	400
GCCTACCTAC	CTTGGCTTCC	ACAAGCAGGT	AAGACAGGTA	CTTCTAACTA	450
TACTGACGAA	GAAATTGAAA	AGTATATCAA	GAATGCTGGT	TACGTAGCTC	500
CAGATGAAAT	GTTTGTGGT	TATACCCGCA	AATATGCAAT	GGCTGTTTGG	550
ACAG					554

## 2) INFORMATION FOR SEQ ID NO: 2060

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1249 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-57

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2060

CAACTGGGAT	GGATGTCTAC	ACAAATGTAG	ACCAAGAAGC	TCAAAAACAT	50
CTGTGGGATA	TTTACAATAC	AGACGAATAC	GTTGCCTATC	CAGACGATGA	100
ATTGCAAGTC	GCTTCTACCA	TTGTTGATGT	TTCTAACGGT	AAAGTCATTG	150
CCCAGCTAGG	AGCACGCCAT	CAGTCAAGTA	ATGTTTCCTT	CGGAATTAAC	200
CAAGCAGTAG	AAACAAACCG	CGACTGGGGA	TCAACTATGA	AACCGATCAC	250
AGACTATGCT	CCTGCCTTGG	AGTACGGTGT	CTACGATTCA	ACTGCTACTA	300
TCGTTACGA	TGAGCCCTAT	AACTACCCTG	GGACAAATAC	TCCTGTTTAT	350
AACTGGGATA	GGGGCTACTT	TGGCAACATC	ACCTTGCAAT	ACGCCCTGCA	400
ACAATCGCGA	AACGTCCCAG	CCGTGGAAAC	TCTAAACAAG	GTCGGACTCA	450
ACCGCGCCAA	GACTTTCCTA	AATGGTCTAG	GAATCGACTA	CCCAAGTATT	500
CACTACTCAA	ATGCCATTTC	AAGTAACACA	ACCGAATCAG	ACAAAAATA	550
TGGAGCAAGT	AGTGAAAAGA	TGGCTGCTGC	TTACGCTGCC	TTTGCAAATG	600
GTGGAACCTA	CTATAAACCA	ATGTATATCC	ATAAAGTCGT	CTTTAGTGAT	650
GGGAGTGAAA	AAGAGTTCTC	TAATGTCGGA	ACTCGTGCCA	TGAAGGAAAC	700
GACAGCCTAT	ATGATGACCG	ACATGATGAA	AACAGTCTTG	ACTTATGGAA	750
CTGGACGAAA	TGCCTATCTT	GCTTGGCTCC	CTCAGGCTGG	TAAAACAGGA	800
ACCTCTAACT	ATACAGACGA	GGAAATTGAA	AACCACATCA	AGACCTCTCA	850
ATTTGTAGCA	CCTGATGAAC	TATTTGCTGG	CTATACGCGT	AAATATTCAA	900
TGGCTGTATG	GACAGGCTAT	TCTAACCGTC	TGACACCACT	TGTAGGCAAT	950
GGCCTTACGG	TCGCTGCCAA	AGTTTACCGC	TCTATGATGA	CCTACCTGTC	1000
TGAAGGAAGC	AATCCAGAAG	ATTGGAATAT	ACCAGAGGGG	CTCTACAGAA	1050
ATGGAGAATT	CGTATTTAAA	AATGGTGCTC	GTTCTACGTG	GAGCTCACCT	1100
GCTCCACAAC	AACCCCATC	AACTGAAAGT	TCAAGCTCAT	CATCAGATAG	1150
TTCAACTTCA	CAGTCTAGCT	CAACCACTCC	AAGCACAAAT	AATAGTACGA	1200
CTACCAATCC	TAACAATAAT	ACGCAACAAT	CAAATACAAC	CCCTGATCA	1249

## 2) INFORMATION FOR SEQ ID NO: 2061

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*  
(B) STRAIN: StrR-60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2061

GAAGTTGAAC	AGACTGGTCA	CCAAGCTCCT	TCATATCCGC	CAACACTGCA	50
ATTTTCTTGC	CACCTTCATT	GGCTGGAATG	GCAGAGAAAG	TCTCTAAAAT	100
CAGTTTCATA	GCAGTTGGAT	TGGCATTATA	AACATCTGAC	AGGATATCTG	150
CTCCATTGGC	TGCTTTCTTC	CACCTCGGTAC	GGTTACGCGT	CAATTCAAGA	200
TGTTGGAAGG	CCAAACGAAT	TTGCTCCTCT	GAAACTCCTT	CTTGCAAGGC	250
AACATAGGAT	GCAATCATAG	CATTTGTCGC	ATTGTACTTG	CCAGTTACTG	300
GCAAATCAAG	GGCTTGCTCT	AAGAAATTGA	CCTTGAAGGT	CAGACTATCT	350
TTGCGCTCAA	CCAAGTCGGT	AATTCCCAGC	TCTGCTCCTT	GACCAAAACG	400
AACCACCTTT	TTATCAGTTG	GCAAATAGTC	CTCTACGATA	GGGTCAGCCG	450
GCGCTAAAAG	CAAGGAACCT	GAAGCCATTC	CGTCTGCAAT	TTGCATTTTT	500
CCTTTAGCAA	TCTCAGAACG	GTCTTTGAAA	AAGGCCAAAT	GAGCTTCTCC	550
AACCAAGGTC	ACGATGGCTG	TATGGACAG			579

## 2) INFORMATION FOR SEQ ID NO: 2062

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1216 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*  
(B) STRAIN: StrR-63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2062

AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
TACCCTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTAG	ATGTTTCAAA	100
TGGTAAAGTC	ATCGCACAAAC	TTGGTGCTCG	TCATCAAGCA	AGTAATGTTT	150
CATTCGGTAC	CAACCAGGCC	GTAGAAACCA	ATCGTGACTG	GGGATCATCA	200
ATGAAACCAA	TCACTGACTA	TGCTCCCGCT	TTAGAATATG	GAGTCTATGA	250
CTCTACTGCT	TCTATTGTAC	ATGATGTCCC	TTATAACTAT	CCTGGCACTG	300
ATACTCCACT	CTACAACTGG	GATCATGTCT	ACTTTGGAAA	CATTACAATC	350
CAGTATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	AGACTTTGAA	400
TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	CTTGGTATCG	450
ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	CACAACTGAA	500
TCCAACAAAA	AATATGGTGC	AAGTAGTGAA	AAAAATGGCTG	CTGCCTACGC	550
TGCTTTTGCT	AATGGTGTA	TTTATCACAA	ACCAATGTAT	ATCAATAAAA	600
TCGTCTTTAG	TGATGGTAGC	GAAAAAGAAT	TTTCTGATGC	TGGTACACGA	650
GCTATGAAAG	AGACTACTGC	CTATATGATG	ACTGAAATGA	TGAAAACGTG	700
TTTAACTTAC	GGAACAGGAC	GTGGAGCCTA	CCTACCATGG	CTTCCACAAG	750

CAGGTAAGAC	AGGTACTTCT	AACTATACTG	ACGAAGAAAT	TGAAAAGTAT	800
ATCAAGAACA	CTGGTTACGT	AGCTCCAGAT	GAAATGTTTG	TAGGGTATAC	850
CCGTAAATAT	GCAATGGCTG	TTTGGACAGG	ATACTCAAAT	CGTCTAACTC	900
CAATCATCGG	AGATGGTTTC	CTTGTTGCTG	GTAAAGTCTA	TCGTTCAATG	950
ATAACTTACC	TTTCTGAAGA	TGACCAACCT	GGAGATTGGA	CAATGCCAGA	1000
TGGCTTGTAT	AGAAATGGAG	AATTCGTATT	TAAAAATGGT	GCTCGTTCTA	1050
CGTGGAGCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	AAGTTCAAGC	1100
TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AGCTCAACCA	CTCCAAGCAC	1150
AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
CAACCCCTGA	TCAACA				1216

## 2) INFORMATION FOR SEQ ID NO: 2063

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: ATCC 700673

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2063

AATACGTCTC	TTACCCTGAC	GATGATTTCG	AAGTCGCATC	CACGGTCGTA	50
GATGTTTCAA	ATGGTAAAGT	CATCGCCCAA	CTTGGAGCTC	GTCACCAAGC	100
AAGTAACGTT	TCATTTGGTA	CCAACCAAGC	TGTGGAAACC	AATCGTGACT	150
GGGGTTCAAC	AATGAAACCC	ATCACCGATT	ATGCACCTGC	CATAGAATAC	200
GGTGTATATG	ATTCCACTGC	AACTATGGTT	AATGATATTC	CTTATAACTA	250
TCCGGGAACA	AGCACACCTG	TCTACAACCTG	GGATCGAGCA	TATTTTGGTA	300
ATATTACTCT	GCAATATGCC	CTTCAACAAT	CTCGTAACGT	ACCCGCCGTT	350
GAGACACTAA	ACAAGGTTGG	TTTAGATAGA	GCTAAAAGTT	TCCTAAATGG	400
TTTAGGAATC	GACTATCCTG	TAATGCACTA	TTCAAATGCT	ATTTCAAGTA	450
ATACTACCGA	ATCTAGTAAA	CAGTACGGGG	CAAGTAGTGA	AAAAATGGCC	500
ACTGCCTATG	CCGCATTCGC	AAACGGCGGT	ATTTACCACA	AACCAATGTA	550
CATCAATAAG	GTTGTCTTTA	GCGATGGTAG	CGAAAAAGAA	TTTTCTGACC	600
CTGGCACAAG	AGCCATGAAA	GAAACGACTG	CTTACATGAT	GACAGAGATG	650
ATGAAAACAG	TCTGGACTTA	CGGAACGGT	CGCGGTGCCT	ACCTACCTTG	700
GCTTCCACAA	GCAGGTAAAA	CAGGTACTTC	TAACATATACT	GACGAAGAAA	750
TTGAAAAGTA	TATCAAGAAC	ACTGGTTACG	TAGCTCCAGA	TGAAATGTTT	800
GTAGGGTATA					810

## 2) INFORMATION FOR SEQ ID NO: 2064

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 782 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*  
(B) STRAIN: ATCC 700678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2064

```

TCTTACCCTG ACGATGATTT GCAAGTCGCA TCTACGGTCG TAGATGTTTC      50
AAATGGTAAA GTCATCGCCC AACTTGGAGC TCGTCACCAA GCAAGTAACG      100
TTTCATTTGG TACCAACCAA GCTGTGGAAA CCAATCGTGA CTGGGGATCA      150
ACTATGAAAC CAATCACAGA CTATGCTCCT GCCTTGGAGT ACGGTGTCTA      200
CGATTCAACT GCTACTATCG TTCACGATGA GCCCTATAAC TACCCTGGGA      250
CAGATATCCC TCTCTATAAC TGGGATCGAG CATATTTTCGG TAATATTACT      300
CTGCAATATG CCCTTCAACA ATCTCGTAAC GTACCTGCCG TTGAAACACT      350
AAACAAGGTC GGTCTAGATA AGGCTAAAC CTTCCTTAAT GGTCTTGGA      400
TCGACTATCC AAGCATGCAT TATGCAAACG CCATTTCAAG TAATACAAC      450
GAATCCAACA AAAAATATGG TGCAAGTAGT GAAAAAATAG CTACCGCCTA      500
TGCCGCATTC GCAAATGGTG GTATTTACCA CAAACCAATG TACATCAATA      550
AAGTTGTCTT TAGCGATGGT AGCGAAAAAG AATTTTCTGA CCCTGGCACA      600
AGAGCCATGA AAGAAACGAC TGCTTACATG ATGACAGAAA TGATGAAAAC      650
AGTCTGGACG TACGGAACGT GTCGTGGTGC CTACCTGCCT TGGCTTCCTC      700
AAGCTGGTAA AACAGGTACC TCTAACTATA CTGACGAAGA AATTGAAAAG      750
TATATCAAGA AACTGGTTA CGTAGCTCCA GA                          782

```

2) INFORMATION FOR SEQ ID NO: 2065

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2065

CCAGGACGTG GAGGCGATCA CA

22

2) INFORMATION FOR SEQ ID NO: 2066

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2066

CACCGACAGC GAGCCGATCA GA

22

## 2) INFORMATION FOR SEQ ID NO: 2067

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2067

AGCTGAGCCA ATTCATGG

18

## 2) INFORMATION FOR SEQ ID NO: 2068

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1068

ATTCATGGAC CAGAACAAC

19

## 2) INFORMATION FOR SEQ ID NO: 2069

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2069

CGCTGTCGGG GTTGACCC

18

## 2) INFORMATION FOR SEQ ID NO: 2070

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1073

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2070

GTTGACCCAC AAGCGCCG

18

2) INFORMATION FOR SEQ ID NO: 2071

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2071

CGACTGTCGG CGCTGGGG

18

2) INFORMATION FOR SEQ ID NO: 2072

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3534 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
- (B) STRAIN: Rv
- (C) ACCESSION NUMBER: L27989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2072

GTGCTGGAAG	GATGCATCTT	GGCAGATTCC	CGCCAGAGCA	AAACAGCCGC	50
TAGTCCTAGT	CCGAGTCGCC	CGCAAAGTTC	CTCGAATAAC	TCCGTACCCG	100
GAGCGCCAAA	CCGGGTCTCC	TTCGCTAAGC	TGCGCGAACC	ACTTGAGGTT	150
CCGGGACTCC	TTGACGTCCA	GACCGATTCC	TTCGAGTGCC	TGATCGGTTC	200
GCCGCGCTGG	CGCGAATCCG	CCGCCGAGCG	GGGTGATGTC	AACCCAGTGG	250
GTGGCCTGGA	AGAGGTGCTC	TACGAGCTGT	CTCCGATCGA	GGACTTCTCC	300
GGGTCGATGT	CGTTGTCTGT	CTCTGACCCT	CGTTTCGACG	ATGTCAAGGC	350
ACCCGTCGAC	GAGTGCAAAG	ACAAGGACAT	GACGTACGCG	GCTCCACTGT	400
TCGTCAACGC	CGAGTTCATC	AACAACAACA	CCGGTGAGAT	CAAGAGTCAG	450
ACGGTGTTCA	TGGGTGACTT	CCCGATGATG	ACCGAGAAGG	GCACGTTCAT	500
CATCAACGGG	ACCGAGCGTG	TGGTGCTCAG	CCAGCTGGTG	CGGTCGCCCCG	550
GGGTGTACTT	CGACGAGACC	ATTGACAAGT	CCACCGACAA	GACGCTGCAC	600
AGCGTCAAGG	TGATCCCGAG	CCGCGGCGCG	TGGCTCGAGT	TTGACGTCGA	650
CAAGCGCGAC	ACCGTCGGCG	TGCGCATCGA	CCGCAAACGC	CGGCAACCCG	700

TCACCGTGCT	GCTCAAGGCG	CTGGGCTGGA	CCAGCGAGCA	GATTGTCGAG	750
CGGTTCCGGT	TCTCCGAGAT	CATGCGATCG	ACGCTGGAGA	AGGACAACAC	800
CGTCGGCACC	GACGAGGCGC	TGTTGGACAT	CTACCGCAAG	CTGCGTCCGG	850
GCGAGCCCCC	GACCAAAGAG	TCAGCGCAGA	CGCTGTTGGA	AAACTTGTTT	900
TTCAAGGAGA	AGCGCTACGA	CCTGGCCCCG	GTCGGTCGCT	ATAAGGTCAA	950
CAAGAAGCTC	GGGCTGCATG	TCGGCGAGCC	CATCACGTCG	TCGACGCTGA	1000
CCGAAGAAGA	CGTCGTGGCC	ACCATCGAAT	ATCTGGTCCG	CTTGACGAG	1050
GGTCAGACCA	CGATGACCGT	TCCGGGCGGC	GTCGAGGTGC	CGGTGGAAAC	1100
CGACGACATC	GACCACTTCG	GCAACCGCCG	CCTGCGTACG	GTCGGCGAGC	1150
TGATCCAAAA	CCAGATCCGG	GTCGGCATGT	CGCGGATGGA	GCGGGTGGTC	1200
CGGGAGCGGA	TGACCACCCA	GGACGTGGAG	GCGATCACAC	CGCAGACGTT	1250
GATCAACATC	CGGCCGGTGG	TCGCCGCGAT	CAAGGAGTTC	TTCGGCACCA	1300
GCCAGCTGAG	CCAATTCATG	GACCAGAACA	ACCCGCTGTC	GGGGTTGACC	1350
CACAAGCGCC	GACTGTCTGG	GCTGGGGCCC	GGCGGTCTGT	CACGTGAGCG	1400
TGCCGGGCTG	GAGGTCCGCG	ACGTGCACCC	GTCGCACTAC	GGCCGGATGT	1450
GCCCCGATCGA	AACCCCTGAG	GGGCCCAACA	TCGGTCTGAT	CGGCTCGCTG	1500
TCGGTGTACG	CGCGGGTCAA	CCCGTTCGGG	TTCATCGAAA	CGCCGTACCG	1550
CAAGGTGGTC	GACGGCGTGG	TTAGCGACGA	GATCGTGTAC	CTGACCGCCG	1600
ACGAGGAGGA	CCGCCACGTG	GTGGCACAGG	CCAATTCGCC	GATCGATCGC	1650
GACGGTCGCT	TCGTGAGGCC	GCGCGTGCTG	GTCCGCCGCA	AGGCGGGCGA	1700
GGTGGAGTAC	GTGCCCTCGT	CTGAGGTGGA	CTACATGGAC	GTCTCGCCCC	1750
GCCAGATGGT	GTCGGTGGCC	ACCGCGATGA	TTCCCTTCCT	GGAGCACGAC	1800
GACGCCAACCC	GTGCCCTCAT	GGGGGCAAAC	ATGCAGCGCC	AGGCGGTGCC	1850
GCTGGTCCGT	AGCGAGGCC	CGCTGGTGGG	CACCGGGATG	GAGCTGCGCG	1900
CGGCGATCGA	CGCGGCGACG	TCGTGCTCGC	AAGAAAGCGG	CGTCATCGAG	1950
GAGGTGTCCG	CCGACTACAT	CACTGTGATG	CACGACAACG	GCACCCGGCG	2000
TACCTACCGG	ATGCGCAAGT	TTGCCCGGTC	CAACCACGGC	ACTTGCGCCA	2050
ACCAAGTGGC	CATCGTGGAC	GCGGGCGACC	GAGTCGAGGC	CGGTGAGGTG	2100
ATCGCCGACG	GTCCCTGTAC	TGACGACGGC	GAGATGGCGC	TGGGCAAGAA	2150
CCTGCTGGTG	GCCATCATGC	CGTGGGAGGG	CCACAACCTAC	GAGGACGCGA	2200
TCATCCTGTC	CAACCGCCTG	GTGGAAGAGG	ACGTGCTCAC	CTCGATCCAC	2250
ATCGAGGAGC	ATGAGATCGA	TGCTCGCGAC	ACCAAGCTGG	GTGCGGAGGA	2300
GATCACCCGC	GACATCCCGA	ACATCTCCGA	CGAGGTGCTC	GCCGACCTGG	2350
ATGAGCGGGG	CATCGTGCGC	ATCGGTGCCG	AGGTTTCGCGA	CGGGGACATC	2400
CTGGTCCGCA	AGGTACCCCC	GAAGGGTGAG	ACCGAGCTGA	CGCCGGAGGA	2450
GCGGCTGCTG	CGTGCCATCT	TCGGTGAGAA	GGCCCGCGAG	GTGCGCGACA	2500
CTTCGCTGAA	GGTGCCGCAC	GGCGAATCCG	GCAAGGTGAT	CGGCATTCCG	2550
GTGTTTTCCC	GCGAGGACGA	GGACGAGTTG	CCGGCCGGTG	TCAACGAGCT	2600
GGTGCCTGTG	TATGTGGCTC	AGAAACGCAA	GATCTCCGAC	GGTGACAAGC	2650
TGGCCGGCCG	GCACGGCAAC	AAGGGCGTGA	TCGGCAAGAT	CCTGCCGGTT	2700
GAGGACATGC	CGTTCCCTTG	CGACGGCAC	CCGGTGGACA	TTATTTTGAA	2750
CACCCACGGC	GTGCCGCGAC	GGATGAACAT	CGGCCAGATT	TTGGAGACCC	2800
ACCTGGGTTG	GTGTGCCAC	AGCGCTGGA	AGGTCGACGC	CGCCAAGGGG	2850
GTTCCGGACT	GGGCCGCCAG	GCTGCCCGAC	GAACTGCTCG	AGGCGCATGC	2900
GAACGCCATT	GTGTGACGCG	CGGTGTTTCA	CGGCGCCAG	GAGGCCGAGC	2950
TGCAGGGCCT	GTTGTGCTGC	ACGCTGCCCA	ACCGCGACGG	TGACGTGCTG	3000
GTCGACGCCG	ACGGCAAGGC	CATGCTCTTC	GACGGGCGCA	GCGGCGAGCC	3050
GTTCCCGTAC	CCGGTCACGG	TTGGCTACAT	GTACATCATG	AAGCTGCACC	3100
ACCTGGTGGA	CGACAAGATC	CACGCCCGCT	CCACCGGGCC	GTAATCGATG	3150
ATCACCCAGC	AGCCGCTGGG	CGGTAAGGCG	CAGTTCGGTG	GCCAGCGGTT	3200
CGGGGAGATG	GAGTGCTGGG	CCATGCAGGC	CTACGGTGCT	GCCTACACCC	3250
TGCAGGAGCT	GTTGACCATC	AAGTCCGATG	ACACCGTCCG	CCGCGTCAAG	3300
GTGTACGAGG	CGATCGTCAA	GGGTGAGAAC	ATCCCGGAGC	CGGGCATCCC	3350
CGAGTCGTTT	AAGGTGCTGC	TCAAAGAACT	GCACTGCTG	TGCCTCAACG	3400
TCGAGGTGCT	ATCGAGTGAC	GGTGCGGCGA	TCGAACTGCG	CGAAGGTGAG	3450
GACGAGGACC	TGGAGCGGGC	CGCGGCCAAC	CTGGGAATCA	ATCTGTCCCG	3500
CAACGAATCC	GCAAGTTTCG	AGGATCTTTC	GTAA		3534

## 2) INFORMATION FOR SEQ ID NO: 2073

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2073

CCGAGCAACA TGATTGAACC ATCCACCAAC TGGCTCGG

38

## 2) INFORMATION FOR SEQ ID NO: 2074

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2074

CCGAGCAACA TGATTGAAGC TTCCACCAAC TGGCTCGG

38

## 2) INFORMATION FOR SEQ ID NO: 2075

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2075

CCGAGCCAGG TTCTGAAGTC TCTGCATTAT TAGGTGCTCG G

41

## 2) INFORMATION FOR SEQ ID NO: 2076

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1076



(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2076

CCGAGCYGAY AACATTTTCA GATTCACCCA RCGCTCGG

39

2) INFORMATION FOR SEQ ID NO: 2077

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2077

CCGAGCAACC GATCCAGCTC CAGCTACGCT CGG

33

2) INFORMATION FOR SEQ ID NO: 2078

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2078

CCGAGCCTTG GTCTTCGGCC AAATGAACGC TCGG

34

2) INFORMATION FOR SEQ ID NO: 2079

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2079

CCGAGCGTTC AGTTACTTCA GTCCAAGCCG GCTCGG

36

## 2) INFORMATION FOR SEQ ID NO: 2080

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2080

CCGAGCCGAA GAGGGCCAAG ATGTCGCTCG G

31

## 2) INFORMATION FOR SEQ ID NO: 2081

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2081

GRATYRTYAA AGTTGGTGAG GAAG

24

## 2) INFORMATION FOR SEQ ID NO: 2082

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2082

CMACTTCATC YCGCTTCGTA CC

22

## 2) INFORMATION FOR SEQ ID NO: 2083

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1078

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2083

CCGCCGATGT TCCGTAAATT ACTTGAIGAA GGTCGAGCCG GCGG

44

2) INFORMATION FOR SEQ ID NO: 2084

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2084

CACGCGTCAA CACCCGTACA AGTCGTCTTT TGC GCGTG

38

2) INFORMATION FOR SEQ ID NO: 2085

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2085

CAA ACTAAAG AACATATCTT GCTA

24

2) INFORMATION FOR SEQ ID NO: 2086

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2086

ATATAATTTG CATCACCTTC AAG

23

## 2) INFORMATION FOR SEQ ID NO: 2087

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2087

TCAGCTCGTG GGATTAGGAG AG

22

## 2) INFORMATION FOR SEQ ID NO: 2088

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2088

AGGCTTCACG CTGTTAGGCT GA

22

## 2) INFORMATION FOR SEQ ID NO: 2089

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2089

ATGCTGAACT TATTGACCTT

20

## 2) INFORMATION FOR SEQ ID NO: 2090

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1080

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2090

CGTTACTGGA GTCGAAATG

19

2) INFORMATION FOR SEQ ID NO: 2091

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2091

CGCGACTTGA GATGGAAGTT AGTGAGCTTC TTGGTCGCG

39

2) INFORMATION FOR SEQ ID NO: 2092

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2092

CGCGACGAAA GAACTTCCTG AAGGTCGTGC AGGTCCAG

38

2) INFORMATION FOR SEQ ID NO: 2093

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2093

TGTTGGCAAT CGAAGACACC

20

## 2) INFORMATION FOR SEQ ID NO: 2094

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2094

TTCAATTTCT TGACCTACTT TCAA

24

## 2) INFORMATION FOR SEQ ID NO: 2095

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2095

CGGTCGGGTT GAACGTGG

18

## 2) INFORMATION FOR SEQ ID NO: 2096

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2096

CGCGACCGGT ACCACGGCCA GTAATCGTGT CGCG

34

## 2) INFORMATION FOR SEQ ID NO: 2097

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1185 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

1082

(A) ORGANISM: *Mycoplasma pneumoniae*  
 (B) STRAIN: ATCC 29342  
 (C) ACCESSION NUMBER: AE000019

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2097

```

ATGGCAAGAG AGAAATTTGA CCGATCTAAA CCCCACGTTA ATGTAGGTAC      50
TATTGGCCAC ATTGACCACG GTAAAACAAC TTAAACAGCA GCTATTTGTA      100
CTGTATTAGC AAAAGAAGGT AAATCAGCTG CTACTCGTTA CGACCAAATC      150
GATAAGGCTC CGGAAGAAAA AGCACGGGGA ATTACGATTA ACTCCGCTCA      200
CGTGAGTAC TCCTCTGACA AGCGTCACTA TGCTCACGTT GACTGTCCAG      250
GACACGCTGA CTACATTAAG AACATGATTA CTGGTGCTGC ACAAATGGAT      300
GGTGCCATTC TAGTAGTTTC AGCAACTGAC AGTGTTATGC CCCAAACCCG      350
TGAACACATT TTGTTGGCCC GCCAAGTGGG TG TGCCACGC ATGGTAGTGT      400
TCCTAAACAA GTGTGACATT GCAACTGATG AAGAAGTGCA AGAGTTAGTA      450
GCAGAAAGAG TACGTGACTT ATTAAC TTCT TACGGCTTTG ATGGCAAGAA      500
CACCCCTATT ATTTATGGTT CTGCACTTAA AGCGCTTGAA GGTGATCCTA      550
AGTGGGAAGC TAAGATCCAT GATTTAATGA ATGCAGTTGA TGAATGGATT      600
CCAACCTCTG AACGTGAAGT GGACAAACCC TTCTTGTTGG CAATCGAAGA      650
CACCATGACG ATTACTGGCC GTGGTACCGT GGTTACCGGT CGGGTTGAAC      700
GTGGTGAATT GAAAGTAGGT CAAGAAATTG AAATCGTTGG TTTACGTCCA      750
ATCCGTAAAG CAGTTGTTAC CGGAATCGAA ATGTTCAAAA AGGAACTTGA      800
TTCAGCAATG GCTGGGGACA ACGCTGGGGT ATTACTCCGT GGTGTGGACC      850
GTAAAGAAGT GGAACGTGGT CAAGTGTTAG CTAAACCAGG TTCGATTAAA      900
CCGCACAAGA AATTTAAAGC GGAAATCTAT GCTTTAAAGA AGGAAGAAGG      950
TGGTCGTCAC ACCGGTTTCT TAAACGGTTA CCGTCCCCAA TTCTACTTCC     1000
GTACTACAGA CGTTACTGGT TCGATTTCCC TACCAGAAAA CACCGAAATG     1050
GTGCTACCAG GTGACAATAC CTCGATTACA GTTGAATAA TTGCACCAAT     1100
TGCTTGTGAA AAAGGTAGTA AGTTCTCCAT CCGTGAAGGT GGTCGAACGG     1150
TTGGTGCTGG TTCAGTCACG GAAGTGCTTG AATAG                          1185
  
```

## 2) INFORMATION FOR SEQ ID NO: 2098

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2098

CTGAGTCACA CCGACAAACG TC

22

## 2) INFORMATION FOR SEQ ID NO: 2099

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2099

CCAGGACTGA ACGGGATACG AA

22

## 2) INFORMATION FOR SEQ ID NO: 2100

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2100

GCGAGACGAT AGGTTGTC

18

## 2) INFORMATION FOR SEQ ID NO: 2101

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2609 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
- (B) STRAIN: H37Rv
- (C) ACCESSION NUMBER: Z79701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2101

CAGCCCGCGA	GCGTAACCTG	GCTGCGATTT	CCGGCGCGGA	TTTTCGCAGT	50
GCGGTTACGC	TCGGAAAGCG	CGGGCCTCGC	CCACGCGGCG	GATGATGTCA	100
GCGGGGTGGT	CCTCGGCGAC	GACCCGGACC	ACGATCCACC	CGTAGCGGTG	150
CTGGACTTTC	TCGTGCCCGA	GGATGTCTTT	CCGGTAGTGG	TAGCGACTGG	200
TCAGATGGTG	GTGCGCGTCA	TACTCGGCCG	CGACCTTGAT	GTCTTGCCAG	250
CCCATATCCA	AATGGGCTTC	CGCCCAGCCC	CATTCGTTGC	GCACCGCGAT	300
CTGCGTCTGG	GGGCGCGGAA	AGCCGGCGCG	GATCAACAAC	AAGCGCAGCC	350
AGGTTTCCTT	GGGGGACTGG	GCACCGCCGT	CGACGAGGTC	CAGAGCGGCT	400
CTTGCGGCCT	TCATGCCACG	GCGGCCCCGA	TAGCGCTCGA	TCAGCGGCTC	450
GACGTCGGCC	ACCTTCAAAT	CGGTGGCCTG	TATCAGGGCG	TCGACGGCCG	500
CGACGGCGGG	GTCCAATGGA	AATCGACTGG	TCAGGTCGAG	CGCCGTTTCG	550
TCCGGTGTGG	TCACGCGCAT	GCCCTCGATG	ACGCAGATCT	CGTCGGGCTC	600
GATGCGCTCT	TCCCAGACTT	GCAGCCCCGG	GGCACGGCGG	CGGTGCGTGT	650
CGATGATCGC	GGCGGGAAGA	TCCGCGTCGA	TCCACTTGGC	GCCATGGAAG	700
GCAGAAGCCG	AGTAGCCGGC	CAGCACGCCG	CGGCGGCGCG	AGCGCAGCCA	750
CAGCGCTTTT	GCACGCAATT	GCGCGGTCAG	TTCCACACCC	TGCGGCACGT	800

1084



ACACGTCTTT	ATGTAGCGCG	ACATACCTGC	TGCGCAATTC	GTAGGGCGTC	850
AATACACCCG	CAGCCAGGGC	CTCGCTGCCC	AGAAAGGGAT	CCGTCATGGT	900
CGAAGTGTGC	TGAGTCACAC	CGACAAACGT	CACGAGCGTA	ACCCCACTGC	950
GAAAGTTCCC	GCCGGAAATC	GCAGCCACGT	TACGCTCGTG	GACATACCGA	1000
TTTCGGCCCC	GCCGCGGCGA	GACGATAGGT	TGTCGGGGTG	ACTGCCACAG	1050
CCACTGAAGG	GGCCAAACCC	CCATTCGTAT	CCCGTTCAGT	CCTGGTTACC	1100
GGAGGAAACC	GGGGGATCGG	GCTGGCGATC	GCACAGCGGC	TGGCTGCCGA	1150
CGGCCACAAG	GTGGCCGTCA	CCCACCGTGG	ATCCGGAGCG	CCAAAGGGGC	1200
TGTTTGGCGT	CGAATGTGAC	GTCACCGACA	GCGACGCCGT	CGATCGCGCC	1250
TTACCGCGG	TAGAAGAGCA	CCAGGGTCCG	GTCGAGGTGC	TGGTGTTCAA	1300
CGCCGGCCTA	TCCGCGGACG	CATTCTCAT	GCGGATGACC	GAGGAAAAGT	1350
TCGAGAAGGT	CATCAACGCC	AACCTCACCG	GGGCGTTCCG	GGTGGCTCAA	1400
CGGGCATCGC	GCAGCATGCA	GCGCAACAAA	TTCGGTCGAA	TGATATTCAT	1450
AGGTTCCGGT	TCCGGCAGCT	GGGGCATCGG	CAACCAGGCC	AACTACGCAG	1500
CCTCCAAGGC	CGGAGTGATT	GGCATGGCCC	GCTCGATCGC	CCGCGAGCTG	1550
TCGAAGGCAA	ACGTGACCGC	GAATGTGGTG	GCCCCGGGCT	ACATCGACAC	1600
CGATATGACC	CGCGCGCTGG	ATGAGCGGAT	TCAGCAGGGG	GCGCTGCAAT	1650
TTATCCCAGC	GAAGCGGGTC	GGCACCCCCG	CCGAGGTCGC	CGGGGTGGTC	1700
AGCTTCCTGG	CTTCCGAGGA	TGCGAGCTAT	ATCTCCGGTG	CGGTCATCCC	1750
GGTCGACGGC	GGCATGGGTA	TGGGCCACTG	ACACAACACA	AGGACGCACA	1800
TGACAGGACT	GCTGGACGGC	AAACGGATTC	TGGTTAGCGG	AATCATCACC	1850
GACTCGTCGA	TCGCGTTTCA	CATCGCACGG	GTAGCCAGG	AGCAGGGCGC	1900
CCAGCTGGTG	CTCACCGGGT	TCGACCGGCT	GCGGCTGATT	CAGCGCATCA	1950
CCGACCGGCT	GCCGGCAAAG	GCCCCGCTGC	TCGAACTCGA	CGTGCAAAAC	2000
GAGGAGCACC	TGGCCAGCTT	GGCCGGCCGG	GTGACCGAGG	CGATCGGGGC	2050
GGGCAACAAG	CTCGACGGGG	TGGTGCAATC	GATTGGGTTT	ATGCCGCAGA	2100
CCGGGATGGG	CATCAACCCG	TTCTTCGACG	CGCCCTACGC	GGATGTGTCC	2150
AAGGGCATCC	ACATCTCGGC	GTATTTCGTAT	GCTTCGATGG	CCAAGGCGCT	2200
GCTGCCGATC	ATGAACCCCG	GAGGTTCCAT	CGTCGGCATG	GACTTCGACC	2250
CGAGCCGGGC	GATGCCGGCC	TACAACTGGA	TGACGGTCGC	CAAGAGCGCG	2300
TTGGAGTCGG	TCAACAGGTT	CGTGGCGCGC	GAGGCCGGCA	AGTACGGTGT	2350
GCGTTTGAAT	CTCGTTGCCG	CAGGCCCTAT	CCGGACGCTG	GCGATGAGTG	2400
CGATCGTCGG	CGGTGCGCTC	GGCGAGGAGG	CCGGCGCCCA	GATCCAGCTG	2450
CTCGAGGAGG	GCTGGGATCA	GCGCGCTCCG	ATCGGCTGGA	ACATGAAGGA	2500
TGCGACGCCG	GTCGCCAAGA	CGGTGTGCGC	GCTGCTGTCT	GACTGGCTGC	2550
CGGCGACCAC	GGGTGACATC	ATCTACGCCG	ACGGCGGCGC	GCACACCCAA	2600
TTGCTCTAG					2609

## 2) INFORMATION FOR SEQ ID NO: 2102

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2102

CACCTTCACC CTGACCGACG

20

## 2) INFORMATION FOR SEQ ID NO: 2103

1085

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2103

CGAACCAGCG GAAATAGTTG GAC

23

## 2) INFORMATION FOR SEQ ID NO: 2104

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2104

CTGGGCATGG CIGGAGTC

18

## 2) INFORMATION FOR SEQ ID NO: 2105

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3297 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
- (B) STRAIN: H37rv
- (C) ACCESSION NUMBER: U68480

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2105

ATGACACAGT	GCGCGAGCAG	ACGCAAAGC	ACCCCAAATC	GGGCGATTTT	50
GGGGGCTTTT	GCGTCTGCTC	GCGGGACGCG	CTGGGTGGCC	ACCATCGCCG	100
GGCTGATTGG	CTTTGTGTTG	TCGGTGGCGA	CGCCGCTGCT	GCCCGTCGTG	150
CAGACCACCG	CGATGCTCGA	CTGGCCACAG	CGGGGGCAAC	TGGGCAGCGT	200
GACCGCCCCG	CTGATCTCGC	TGACGCCGGT	CGACTTTACC	GCCACCGTGC	250
CGTGCGACGT	GGTGCGCGCC	ATGCCACCCG	CGGGCGGGGT	GGTGCTGGGC	300
ACCGCACCCA	AGCAAGGCAA	GGACGCCAAT	TTGCAGGCGT	TGTTCTGTCG	350
CGTCAGCGCC	CAGCGCGTGG	ACGTCACCGA	CCGCAACGTG	GTGATCTTGT	400
CCGTGCCGCG	CGAGCAGGTG	ACGTCCCCCG	AGTGTCACG	CATCGAGGTC	450

1086

ACCTCTACCC	ACGCCGGCAC	CTTCGCCAAC	TTCGTCGGGC	TCAAGGACCC	500
GTCGGGCGCG	CCGCTGCGCA	GCGGCTTCCC	CGACCCCAAC	CTGCGCCCGC	550
AGATTGTCGG	GGTGTTCACC	GACCTGACCG	GGCCCGCGCC	GCCCGGGCTG	600
GCGGTCTCGG	CGACCATCGA	CACCCGGTTC	TCCACCCGGC	CGACCACGCT	650
GAAACTGCTG	GCGATCATCG	GGGCGATCGT	GGCCACCGTC	GTCGCACTGA	700
TCGCGTTGTG	GCGCCTGGAC	CAGTTGGACG	GGCGGGGCTC	AATTGCCCAG	750
CTCCTCCTCA	GGCCGTTCCG	GCCTGCATCG	TGCGCGGGCG	GCATGCGCCG	800
GCTGATTCCG	GCAAGCTGGC	GCACCTTCAC	CCTGACCGAC	GCCGTGGTGA	850
TATTCGGCTT	CCTGCTCTGG	CATGTCATCG	GCGCGAATTC	GTCGGACGAC	900
GGCTACATCC	TGGGCATGGC	CCGAGTCGCC	GACCACGCCG	GCTACATGTC	950
CAACTATTTC	CGCTGGTTTC	GCAGCCCGGA	GGATCCCTTC	GGCTGGTATT	1000
ACAACCTGCT	GGCGCTGATG	ACCCATGTCA	GCGACGCCAG	TCTGTGGATG	1050
CGCCTGCCAG	ACCTGGCCGC	CGGGCTAGTG	TGCTGGCTGC	TGCTGTGCGG	1100
TGAGGTGCTG	CCCCGCCTCG	GGCCGGCGGT	GGAGGCCAGC	AAACCCGCCT	1150
ACTGGGCGGC	GGCCATGGTC	TTGCTGACCG	CGTGGATGCC	GTTCAACAAC	1200
GGCCTGCGGC	CGGAGGGCAT	CATCGCGCTC	GGCTCGCTGG	TCACCTATGT	1250
GCTGATCGAG	CGGTCCATGC	GGTACAGCCG	GCTCACACCG	GCGGCGCTGG	1300
CCGTCGTTAC	CGCCGCATTC	ACACTGGGTG	TGCAGCCAC	CGGCCTGATC	1350
GCGGTGGCCG	CGCTGGTGGC	CGGCGGCCGC	CCGATGCTGC	GGATCTTGTT	1400
GCGCCGYCAT	CGCCTGGTCG	GCACGTTGCC	GTTGGTGTGC	CCGATGCTGG	1450
CCGCCGGCAC	CGTCATCCTG	ACCGTGGTGT	TCGCCGACCA	GACCCTGTCA	1500
ACGGTGTGTT	AAGCCACCAG	GGTTCGCGCC	AAAATCGGGC	CGAGCCAGGC	1550
GTGGTATACC	GAGAACCTGC	GTTACTACTA	CCTCATCCTG	CCCACCGTCG	1600
ACGGTTCGCT	GTCGCGGCGC	TTCGGCTTTT	TGATCACCGC	GCTATGCCTG	1650
TTCACCGCGG	TGTTTCATCAT	GTTGCGGCGC	AAGCGAATTC	CCAGCGTGGC	1700
CCGCGGACCG	GCGTGGCGGC	TGATGGGCGT	CATCTTCGGC	ACCATGTTCT	1750
TCCTGATGTT	CACGCCCACC	AAGTGGGTGC	ACCACTTCGG	GCTGTTTCGCC	1800
GCCGTAGGGG	CGGCGATGGC	CGCGCTGACG	ACGGTGTGTT	TATCCCCATC	1850
GGTGCTGCGC	TGGTCGCGCA	ACCGGATGGC	GTTCTTGCGG	GCGTTATTCT	1900
TCCTGCTGGC	GTTGTGTTGG	GCCACCACCA	ACGGCTGGTG	GTATGTCTCC	1950
AGCTACGGTG	TGCCGTTCAA	CAGCGCGATG	CCGAAGATCG	ACGGGATCAC	2000
AGTCAGCACA	ATCTTTTTCG	CCCTGTTTGC	GATCGCCGCC	GGCTATGCGG	2050
CCTGGCTGCA	CTTCGCGCCC	CGCGGCGCCG	GCGAAGGGCG	GCTGATCCGC	2100
GCGCTGACGA	CAGCCCCGGT	ACCGATCGTG	GCCGGTTTCA	TGGCGGCGGT	2150
GTTTCGTGCG	TCCATGGTGG	CCGGGATCGT	GCGACAGTAC	CCGACCTACT	2200
CCAACGGCTG	GTCCAACGTG	CGGGCGTTTG	TCGGCGGCTG	CGGACTGGCC	2250
GACGACGTAC	TCGTGAGGCC	TGATACCAAT	GCGGGTTTCA	TGAAGCCGCT	2300
GGACGGCGAT	TCGGGTTCTT	GGGGCCCTTT	GGGCCCCTG	GGTGGAGTCA	2350
ACCCGGTCCG	CTTCACGCCC	AACGGCGTAC	CGGAACACAC	GGTGGCCGAG	2400
GCGATCGTGA	TGAAACCCAA	CCAGCCCGGC	ACCGACTACG	ACTGGGATGC	2450
GCCGACCAAG	CTGACGAGTC	CTGGCATCAA	TGTTTCTACG	GTGCCGCTGC	2500
CCTATGGGCT	CGATCCCGCC	CGGGTACCGT	TGGCAGGCAC	CTACACCACC	2550
GGCGCACAGC	AACAGAGCAC	ACTCGTCTCG	GCGTGGTATC	TCCTGCCTAA	2600
GCCGGACGAC	GGGCATCCGC	TGGTCGTGGT	GACCGCCGCG	GGCAAGATCG	2650
CCGGCAACAG	CGTGCTGCAC	GGGTACACCC	CCGGGCAGAC	TGTGGTGTCT	2700
GAATACGCCA	TGCCGGGACC	CGGAGCGCTG	GTACCCGCGG	GGCGGATGGT	2750
GCCCCGACGAC	CTATACGGAG	AGCAGCCCAA	GGCGTGGCGC	AACCTGCGCT	2800
TCGCCCCGAGC	AAAGATGCCC	GCCGATGCCG	TCGCGGTCCG	GGTGGTGGCC	2850
GAGGATCTGT	CGCTGACACC	GGAGGACTGG	ATCGCGGTGA	CCCCGCCGCG	2900
GGTACCGGAC	CTGCGCTCAC	TGCAGGAATA	TGTGGGCTCG	ACGCAGCCGG	2950
TGCTGCTGGA	CTGGGCGGTC	GGTTTGGCCT	TCCCGTGCCA	GCAGCCGATG	3000
CTGCACGCCA	ATGGCATCGC	CGAAATCCCG	AAGTTCCGCA	TCACACCGGA	3050
CTACTCGGCT	AAGAAGCTGG	ACACCGACAC	GTGGGAAGAC	GGCACTAACG	3100
GCGGCCTGCT	CGGGATCACC	GACCTGTTGC	TGCGGGCCCA	CGTCATGGCC	3150
ACCTACCTGT	CCCGCGACTG	GGCCCGCGAT	TGGGGTTCCC	TGCGCAAGTT	3200
CGACACCCTG	GTCGATGCCC	CTCCCGCCCA	GCTCGAGTTG	GGCACC CGA	3250
CCCGCAGCGG	CCTGTGGTCA	CCGGGCAAGA	TCCGAATTGG	TCCATAG	3297

## 2) INFORMATION FOR SEQ ID NO: 2106

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2106

GCGAGCAGAG CACGCCCTCC TCGCCGCTCG C

31

## 2) INFORMATION FOR SEQ ID NO: 2107

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2107

GCGAGCTCCC CATCTCTGGT TGGCAGCTC GC

32

## 2) INFORMATION FOR SEQ ID NO: 2108

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2108

GCGGGCAACT TCRTCAAGAA GGTTGGTTAC AACCCGCCCG C

41

## 2) INFORMATION FOR SEQ ID NO: 2109

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

1088

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2109

GCGGGCCCAA TCTCTGGTTG GAAYGGTGAC AAGCCCGC

38

2) INFORMATION FOR SEQ ID NO: 2110

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2110

GCGGGCCCTT AACGATTTCA GCGAATCTGG ATTCAGCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2111

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2111

GCGGGCATGA TTGAAGCCAC CACCAACGCT TCCTGGCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2112

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2112

GCGGGCTTGA TGAAGTTTTG GGTTCCTTG ACAATTGCC CGC

43

2) INFORMATION FOR SEQ ID NO: 2113

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2113

GCGGGCACAA GGGTTGGACT AAGGAAACCA AGGCAGCCCCG C

41

## 2) INFORMATION FOR SEQ ID NO: 2114

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2114

GCGGGCATCG ATGCTATTGA ACCACCTGTC AGACCGCCCCG C

41

## 2) INFORMATION FOR SEQ ID NO: 2115

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2115

GCGGGCTTGA TGATTCCTC GAATCTAGAT TGGGCCCCG

39

## 2) INFORMATION FOR SEQ ID NO: 2116

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2116

GCGGGCGGTA AGTCCACCGG TAAGACCTTG TTGGCCCCG

39

1090

## 2) INFORMATION FOR SEQ ID NO: 2117

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2117

GCGGGCGACG CCATTGAGCC ACCTTCGAGA GCCCCG

36

## 2) INFORMATION FOR SEQ ID NO: 2118

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2118

GCGGGCTCCT TGACAATTTC TTCGTATCTG TTCTTGCCCC GC

42

## 2) INFORMATION FOR SEQ ID NO: 2119

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2119

GCGGGCTTAC AACCCTAAGG CTGTTCCATT CGTTGCCCGC

40

## 2) INFORMATION FOR SEQ ID NO: 2120

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1091

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2120

GCGGGCAGAA ACCAAGGCTG GTAAGGTTAC CGGTAGCCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2121

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2121

CGACCGCIAG CCGCACACCA AGTTCCGGTC G

31

2) INFORMATION FOR SEQ ID NO: 2122

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2122

CCGAGCGAAT GTAGGAGTCC AGGGTCTCTG CTCGG

35

2) INFORMATION FOR SEQ ID NO: 2123

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2123

TCTACCACTG AAGCATTAC

19



## 2) INFORMATION FOR SEQ ID NO: 2124

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2124

TAGGTACTGT AGGTTTATTG

20

## 2) INFORMATION FOR SEQ ID NO: 2125

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2125

CACGCGGATT TTGAATCTCT TCCTCTAGTA GCGCGTG

37

## 2) INFORMATION FOR SEQ ID NO: 2126

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2126

ATATCAGAGA CTGATGAG

18

## 2) INFORMATION FOR SEQ ID NO: 2127

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1093

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2127

TAGCATATTC AGAGAATATT GT

22

## 2) INFORMATION FOR SEQ ID NO: 2128

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2128

CAACGCTGGA GAATCTATAT TTGTAGAAAC TGC GTTG

37

## 2) INFORMATION FOR SEQ ID NO: 2129

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8133 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: VPI 10463
- (C) ACCESSION NUMBER: X51797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2129

ATGTCTTTAA	TATCTAAAGA	AGAGTTAATA	AAACTCGCAT	ATAGCATTAG	50
ACCAAGAGAA	AATGAGTATA	AACTATACT	AACTAATTTA	GACGAATATA	100
ATAAGTTAAC	TACAAACAAT	AATGAAAATA	AATATTTGCA	ATTAAAAAAA	150
CTAAATGAAT	CAATTGATGT	TTTTATGAAT	AAATATAAAA	CTTCAAGCAG	200
AAATAGAGCA	CTCTCTAATC	TAAAAAAGA	TATATTAAAA	GAAGTAATTC	250
TTATTAAAAA	TTCCAATACA	AGCCCTGTAG	AAAAAAATTT	ACATTTTGTA	300
TGGATAGGTG	GAGAAGTCAG	TGATATTGCT	CTTGAATACA	TAAAACAATG	350
GGCTGATATT	AATGCAGAAT	ATAATATTAA	ACTGTGGTAT	GATAGTGAAG	400
CATTCTTAGT	AAATACACTA	AAAAAGGCTA	TAGTTGAATC	TTCTACCACT	450
GAAGCATTAC	AGCTACTAGA	GGAAGAGATT	CAAAATCCTC	AATTTGATAA	500
TATGAAATTT	TACAAAAAAA	GGATGGAATT	TATATATGAT	AGACAAAAAA	550
GGTTTATAAA	TTATTATAAA	TCTCAAATCA	ATAAACCTAC	AGTACCTACA	600
ATAGATGATA	TTATAAAGTC	TCATCTAGTA	TCTGAATATA	ATAGAGATGA	650
AACTGTATTA	GAATCATATA	GAACAAATTC	TTTGAGAAAA	ATAAATAGTA	700
ATCATGGGAT	AGATATCAGG	GCTAATAGTT	TGTTTACAGA	ACAAGAGTTA	750
TTAAATATTT	ATAGTCAGGA	GTTGTAAAT	CGTGGAATTT	TAGCTGCAGC	800

1094

ATCTGACATA	GTAAGATTAT	TAGCCCTAAA	AAATTTTGGC	GGAGTATATT	850
TAGATGTTGA	TATGCTTCCA	GGTATTCAC	CTGATTTATT	TAAAACAATA	900
TCTAGACCTA	GCTCTATTGG	ACTAGACCGT	TGGGAAATGA	TAAAATTAGA	950
GGCTATTATG	AAGTATAAAA	AATATATAAA	TAATTATACA	TCAGAAAAC	1000
TTGATAAACT	TGATCAACAA	TTAAAAGATA	ATTTTAAACT	CATTATAGAA	1050
AGTAAAAGTG	AAAAATCTGA	GATATTTTCT	AAATTAGAAA	ATTTAAATGT	1100
ATCTGATCTT	GAAATTAAAA	TAGCTTTCGC	TTTAGGCAGT	GTTATAAATC	1150
AAGCCTTGAT	ATCAAAACAA	GGTTCATATC	TTACTAACCT	AGTAATAGAA	1200
CAAGTAAAAA	ATAGATATCA	ATTTTTTAAAC	CAACACCTTA	ACCCAGCCAT	1250
AGAGTCTGAT	AATAACTTCA	CAGATACTAC	TAAAATTTTT	CATGATTCAT	1300
TATTTAATTC	AGCTACCGCA	GAAAACTCTA	TGTTTTTAAAC	AAAAATAGCA	1350
CCATACTTAC	AAGTAGGTTT	TATGCCAGAA	GCTCGCTCCA	CAATAAGTTT	1400
AAGTGGTCCA	GGAGCTTATG	CGTCAGCTTA	CTATGATTTT	ATAAATTTAC	1450
AAGAAAATAC	TATAGAAAAA	ACTTTTAAAG	CATCAGATTT	AATAGAATTT	1500
AAATTCCCAG	AAAATAATCT	ATCTCAATTG	ACAGAACAAG	AAATAAATAG	1550
TCTATGGAGC	TTTGATCAAG	CAAGTGCAAA	ATATCAATTT	GAGAAATATG	1600
TAAGAGATTA	TACTGGTGGG	TCTCTTTCTG	AAGACAATGG	GGTAGACTTT	1650
AATAAAAAATA	CTGCCCTCGA	CAAAAACTAT	TTATTAAATA	ATAAAATTCC	1700
ATCAACAAT	GTAGAAGAAG	CTGGAAGTAA	AAATTATGTT	CATTATATCA	1750
TACAGTTACA	AGGAGATGAT	ATAAGTTATG	AAGCAACATG	CAATTTATTT	1800
TCTAAAAATC	CTAAAAATAG	TATTATTATA	CAACGAAATA	TGAATGAAAG	1850
TGCAAAAAGC	TACTTTTTAA	GTGATGATGG	AGAATCTATT	TTAGAATTAA	1900
ATAAATATAG	GATACCTGAA	AGATTAAAAA	ATAAGGAAAA	AGTAAAAGTA	1950
ACCTTTTATTG	GACATGGTAA	AGATGAATTC	AACACAAGCG	AATTTGCTAG	2000
ATTAAGTGTA	GATTCACTTT	CCAATGAGAT	AAGTTCATTT	TTAGATACCA	2050
TAAAATTAGA	TATATCACCT	AAAAATGTAG	AAGTAAACTT	ACTTGGATGT	2100
AATATGTTTA	GTTATGATTT	TAATGTTGAA	GAAACTTATC	CTGGGAAGTT	2150
GCTATTAAGT	ATTATGGACA	AAATTACTTC	CACCTTACCT	GATGTAAATA	2200
AAAATTCTAT	TACTATAGGA	GCAAATCAAT	ATGAAGTAAG	AATTAATAGT	2250
GAGGGAAGAA	AAGAACTTCT	GGCTCACTCA	GGTAAATGGA	TAAATAAAGA	2300
AGAAGCTATT	ATGAGCGATT	TATCTAGTAA	AGAATACATT	TTTTTTGATT	2350
CTATAGATAA	TAAGCTAAAA	GCAAAGTCCA	AGAATATTCC	AGGATTAGCA	2400
TCAATATCAG	AAGATATAAA	AACATTATTA	CTTGATGCAA	GTGTTAGTCC	2450
TGATACAAAA	TTTATTTTAA	ATAATCTTAA	GCTTAATATT	GAATCTTCTA	2500
TTGGGGATTA	CATTTATTAT	GAAAAATTAG	AGCCTGTTAA	AAATATAATT	2550
CACAATTCTA	TAGATGATTT	AATAGATGAG	TTCAATCTAC	TTGAAAATGT	2600
ATCTGATGAA	TTATATGAAT	TAAAAAAATT	AAATAATCTA	GATGAGAAGT	2650
ATTTAATATC	TTTTGAAGAT	ATCTCAAAAA	ATAATTCAAC	TTACTCTGTA	2700
AGATTTATTA	ACAAAAGTAA	TGGTGAGTCA	GTTTATGTAG	AAACAGAAAA	2750
AGAAATTTTT	TCAAAATATA	GCGAACATAT	TACAAAAGAA	ATAAGTACTA	2800
TAAAGAATAG	TATAATTACA	GATGTTAATG	GTAATTTATT	GGATAATATA	2850
CAGTTAGATC	ATACTTCTCA	AGTTAATACA	TTAAACGCAG	CATTCTTTAT	2900
TCAATCATTA	ATAGATTATA	GTAGCAATAA	AGATGTACTG	AATGATTTAA	2950
GTACCTCAGT	TAAGGTTCAA	CTTTATGCTC	AACATTTTAG	TACAGGTTTA	3000
AATACTATAT	ATGACTCTAT	CCAATTAGTA	AATTTAATAT	CAAATGCAGT	3050
AAATGATACT	ATAAATGTAC	TACCTACAAT	AACAGAGGGG	ATACCTATTG	3100
TATCTACTAT	ATTAGACGGA	ATAAACTTAG	GTGCAGCAAT	TAAGGAATTA	3150
CTAGACGAAC	ATGACCCATT	ACTAAAAAAA	GAATTAGAAG	CTAAGGTGGG	3200
TGTTTTAGCA	ATAAATATGT	CATTATCTAT	AGCTGCAACT	GTAGCTTCAA	3250
TTGTTGGAAT	AGGTGCTGAA	GTTACTATTT	TCTTATTACC	TATAGCTGGT	3300
ATATCTGCAG	GAATACCTTC	ATTAGTTAAT	AATGAATTAA	TATTGCATGA	3350
TAAGGCAACT	TCAGTGGTAA	ACTATTTTAA	TCATTTGTCT	GAATCTAAAA	3400
AATATGGCCC	TCTTAAAACA	GAAGATGATA	AAATTTTAGT	TCCTATTGAT	3450
GATTTAGTAA	TATCAGAAAT	AGATTTTAAT	AATAATTCGA	TAAAACTAGG	3500
AACATGTAAT	ATATTAGCAA	TGGAGGGGGG	ATCAGGACAC	ACAGTGACTG	3550
GTAATATAGA	TCACCTTTTC	TCATCTCCAT	CTATAAGTTC	TCATATTCCT	3600
TCATTATCAA	TTTATTCTGC	AATAGGTATA	GAAACAGAAA	ATCTAGATTT	3650

TTCAAAAAAA	ATAATGATGT	TACCTAATGC	TCCTTCAAGA	GTGTTTTTGGT	3700
GGGAAACTGG	AGCAGTTCCA	GGTTTAAGAT	CATTGGAAAA	TGACGGAAC	3750
AGATTACTTG	ATTCAATAAG	AGATTTTATAC	CCAGGTAAAT	TTTACTGGAG	3800
ATTCTATGCT	TTTTTCGATT	ATGCAATAAC	TACATTAAAA	CCAGTTTATG	3850
AAGACACTAA	TATTAATAAT	AAACTAGATA	AAGATACTAG	AAACTTCATA	3900
ATGCCAACTA	TAACACTATA	CGAAATTAGA	AACAAATTAT	CTTATTCATT	3950
TGATGGAGCA	GGAGGAACTT	ACTCTTTATT	ATTATCTTCA	TATCCAATAT	4000
CAACGAATAT	AAATTTATCT	AAAGATGATT	TATGGATATT	TAATATTGAT	4050
AATGAAGTAA	GAGAAATATC	TATAGAAAAT	GGTACTATTA	AAAAAGGAAA	4100
GTTAATAAAA	GATGTTTTAA	GTAAAATTGA	TATAAATAAA	AATAAACTTA	4150
TTATAGGCAA	TCAAACAATA	GATTTTTTCAG	GCGATATAGA	TAATAAAGAT	4200
AGATATATAT	TCTTGACTTG	TGAGTTAGAT	GATAAAATTA	GTTTAATAAT	4250
AGAAATAAAT	CTTGTTGCAA	AATCTTATAG	TTTGTTATTG	TCTGGGGATA	4300
AAAATTATTT	GATATCCAAT	TTATCTAATA	CTATTGAGAA	AATCAATACT	4350
TTAGGCCTAG	ATAGTAAAAA	TATAGCGTAC	AATTACACTG	ATGAATCTAA	4400
TAATAAATAT	TTTGAGGCTA	TATCTAAAAC	AAGTCAAAAA	AGCATAATAC	4450
ATTATAAAAA	AGACAGTAAA	AATATATTAG	AATTTTATAA	TGACAGTACA	4500
TTAGAATTTA	ACAGTAAAGA	TTTTATTGCT	GAAGATATAA	ATGTATTTAT	4550
GAAAGATGAT	ATTAATACTA	TAACAGGAAA	ATACTATGTT	GATAATAATA	5000
CTGATAAAAG	TATAGATTTT	TCTATTTCTT	TAGTTAGTAA	AAATCAAGTA	5050
AAAGTAAATG	GATTATATTT	AAATGAATCC	GTATACTCAT	CTTACCTTGA	5100
TTTTGTGAAA	AATTCAGATG	GACACCATAA	TACTTCTAAT	TTTATGAATT	5150
TATTTTTTGA	CAATATAAGT	TTCTGGAAAT	TGTTTGGGTT	TGAAAATATA	5200
AATTTTGTAA	TCGATAAATA	CTTTACCCTT	GTTGGTAAAA	CTAATCTTGG	5250
ATATGTAGAA	TTTATTTGTG	ACAATAATAA	AAATATAGAT	ATATATTTTG	5300
GTGAATGGAA	AACATCGTCA	TCTAAAAGCA	CTATATTTAG	CGGAAATGGT	5350
AGAAATGTTG	TAGTAGAGCC	TATATATAAT	CCTGATACGG	GTGAAGATAT	5400
ATCTACTTCA	CTAGATTTTT	CCTATGAACC	TCTCTATGGA	ATAGATAGAT	5450
ATATAAATAA	AGTATTGATA	GCACCTGATT	TATATACAAG	TTTAATAAAT	5500
ATTAATACCA	ATTATTATTC	AAATGAGTAC	TACCCTGAGA	TTATAGTTCT	5550
TAACCCAAAT	ACATTCCACA	AAAAAGTAAA	TATAAATTTA	GATAGTTCTT	5600
CTTTTGAGTA	TAAATGGTCT	ACAGAAGGAA	GTGACTTTAT	TTTAGTTAGA	5650
TACTTAGAAG	AAAGTAATAA	AAAAATATTA	CAAAAAATAA	GAATCAAAGG	5700
TATCTTATCT	AATACTCAAT	CATTTAATAA	AATGAGTATA	GATTTTAAAG	5750
ATATTAAAAA	ACTATCATT	GGATATATAA	TGAGTAATTT	TAAATCATT	5800
AATTCTGAAA	ATGAATTAGA	TAGAGATCAT	TTAGGATTTA	AAATAATAGA	5850
TAATAAAACT	TATTACTATG	ATGAAGATAG	TAAATTAGTT	AAAGGATTAA	5900
GCAAGTAATT	GACAATAATA	AGTATTATTT	CAATCCTGAC	ACTGCTATCA	5950
TCTCAAAAGG	TTGGCAGACT	GTTAATGGTA	GTAGATACTA	CTTTGATACT	6000
GATACCGCTA	TTGCCTTTAA	TGGTTATAAA	ACTATTGATG	GTAAACACTT	6050
TTATTTTGAT	AGTGATTGTG	TAGTGAAAAT	AGGTGTGTTT	AGTACCTCTA	6100
ATGGATTTGA	ATATTTTGCA	CCTGCTAATA	CTTATAATAA	TAACATAGAA	6150
GGTCAGGCTA	TAGTTTATCA	AAGTAAATTC	TTAACTTTGA	ATGGTAAAAA	6200
ATATTACTTT	GATAATAACT	CAAAAGCAGT	TACCGGATTG	CAAACATTG	6250
ATAGTAAAAA	ATATTACTTT	AATACTAACA	CTGCTGAAGC	AGCTACTGGA	6300
TGGCAAACTA	TTGATGGTAA	AAAATATTAC	TTTAATACTA	ACACTGCTGA	6350
AGCAGCTACT	GGATGGCAAA	CTATTGATGG	TAAAAAATAT	TACTTTAATA	6400
CTAACACTGC	TATAGCTTCA	ACTGGTTATA	CAATTATTAA	TGGTAAACAT	6450
TTTTATTTTA	ATACTGATGG	TATTATGCAG	ATAGGAGTGT	TTAAAGGACC	6500
TAATGGATTT	GAATATTTTG	CACCTGCTAA	TACGGATGCT	AACAACATAG	6550
AAGGTCAAGC	TATACTTTAC	CAAAATGAAT	TCTTAACCTT	GAATGGTAAA	6600
AAATATTACT	TTGGTAGTGA	CTCAAAAGCA	GTTACTGGAT	GGAGAATTAT	6650
TAACAATAAG	AAATATTACT	TTAATCCTAA	TAATGCTATT	GCTGCAATTC	6700
ATCTATGCAC	TATAAATAAT	GACAAGTATT	ACTTTAGTTA	TGATGGAATT	6750
CTTCAAAATG	GATATATTAC	TATTGAAAGA	AATAATTTCT	ATTTTGATGC	6800
TAATAATGAA	TCTAAAATGG	TAACAGGAGT	ATTAAAGGA	CCTAATGGAT	6850
TTGAGTATTT	TGCACCTGCT	AATACTCACA	ATAATAACAT	AGAAGGTCAG	6900

GCTATAGTTT	ACCAGAACAA	ATTCTTAACT	TTGAATGGCA	AAAAATATTA	6950
TTTTGATAAT	GACTCAAAAG	CAGTTACTGG	ATGGCAAACC	ATTGATGGTA	7000
AAAAATATTA	CTTTAATCTT	AACACTGCTG	AAGCAGCTAC	TGGATGGCAA	7050
ACTATTGATG	GTAAAAAATA	TTACTTTAAT	CTTAACACTG	CTGAAGCAGC	7100
TACTGGATGG	CAAACTATTG	ATGGTAAAAA	ATATTACTTT	AATACTAACA	7150
CTTTCATAGC	CTCAACTGGT	TATACAAGTA	TTAATGGTAA	ACATTTTTTAT	7200
TTTAATACTG	ATGGTATTAT	GCAGATAGGA	GTGTTTAAAG	GACCTAATGG	7250
ATTTGAATAC	TTTGCACCTG	CTAATACGGA	TGCTAACAAAC	ATAGAAGGTC	7300
AAGCTATACT	TTACCAAAAT	AAATTCTTAA	CTTTGAATGG	TAAAAAATAT	7350
TACTTTGGTA	GTGACTCAAA	AGCAGTTACC	GGACTGCGAA	CTATTGATGG	7400
TAAAAAATAT	TACTTTAATA	CTAACACTGC	TGTTGCAGTT	ACTGGATGGC	7450
AAACTATTAA	TGGTAAAAAA	TACTACTTTA	ATACTAACAC	TTCTATAGCT	7500
TCAACTGGTT	ATACAATTAT	TAGTGGTAAA	CATTTTTTATT	TTAATACTGA	7550
TGGTATTATG	CAGATAGGAG	TGTTTAAAGG	ACCTGATGGA	TTTGAATACT	7600
TTGCACCTGC	TAATACAGAT	GCTAACAATA	TAGAAGGTCA	AGCTATACGT	7650
TATCAAAATA	GATTCCCTATA	TTTACATGAC	AATATATATT	ATTTTGGTAA	7700
TAATTCAAAA	GCGGCTACTG	GTTGGGTAAC	TATTGATGGT	AATAGATATT	7750
ACTTCGAGCC	TAATACAGCT	ATGGGTGCGA	ATGGTTATAA	AACTATTGAT	7800
AATAAAAAAT	TTTACTTTAG	AAATGGTTTA	CCTCAGATAG	GAGTGTTTAA	7850
AGGGTCTAAT	GGATTTGAAT	ACTTTGCACC	TGCTAATACG	GATGCTAACA	7900
ATATAGAAGG	TCAAGCTATA	CGTTATCAAA	ATAGATTCCT	ACATTTACTT	7950
GGAAAAATAT	ATTACTTTGG	TAATAATTCA	AAAGCAGTTA	CTGGATGGCA	8000
AACTATTAAT	GGTAAAGTAT	ATTACTTTAT	GCCTGATACT	GCTATGGCTG	8050
CAGCTGGTGG	ACTTTTCGAG	ATTGATGGTG	TTATATATTT	CTTTGGTGTT	8100
GATGGAGTAA	AAGCCCCTGG	GATATATGGC	TAA		8133

## 2) INFORMATION FOR SEQ ID NO: 2130

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7101 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: VPI 10463
- (C) ACCESSION NUMBER: X53138

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2130

ATGAGTTTAG	TTAATAGAAA	ACAGTTAGAA	AAAATGGCAA	ATGTAAGATT	50
TCGTACTCAA	GAAGATGAAT	ATGTTGCAAT	ATTGGATGCT	TTAGAAGAAT	100
ATCATAATAT	GTCAGAGAAT	ACTGTAGTCG	AAAAATATTT	AAAATTAAAA	150
GATATAAATA	GTTTAACAGA	TATTTATATA	GATACATATA	AAAAATCTGG	200
TAGAAATAAA	GCCTTAAAAA	AATTTAAGGA	ATATCTAGTT	ACAGAAGTAT	250
TAGAGCTAAA	GAATAATAAT	TTAACTCCAG	TTGAGAAAAA	TTTACATTTT	300
GTTTGGATTG	GAGGTCAAAT	AAATGACACT	GCTATTAATT	ATATAAATCA	350
ATGGAAAGAT	GTAAATAGTG	ATTATAATGT	TAATGTTTTT	TATGATAGTA	400
ATGCATTTT	GATAAACACA	TTGAAAAAAA	CTGTAGTAGA	ATCAGCAATA	450
AATGATACAC	TTGAATCATT	TAGAGAAAAC	TTAAATGACC	CTAGATTTGA	500
CTATAATAAA	TTCTTCAGAA	AACGTATGGA	AATAATTTAT	GATAAACAGA	550
AAAATTTT	CACTACTAT	AAAGCTCAAA	GAGAAGAAAA	TCCTGAACCTT	600

ATAATTGATG	ATATTGTAAA	GACATATCTT	TCAAATGAGT	ATTCAAAGGA	650
GATAGATGAA	CTTAATACCT	ATATTGAAGA	ATCCTTAAAT	AAAAATTACAC	700
AGAATAGTGG	AAATGATGTT	AGAAACTTTG	AAGAATTTAA	AAATGGAGAG	750
TCATTCAACT	TATATGAACA	AGAGTTGGTA	GAAAGGTGGA	ATTTAGCTGC	800
TGCTTCTGAC	ATATTAAGAA	TATCTGCATT	AAAAGAAATT	GGTGGTATGT	850
ATTTAGATGT	TGATATGTTA	CCAGGAATAC	AACCAGACTT	ATTTGAGTCT	900
ATAGAGAAAC	CTAGTTCAGT	AACAGTGGAT	TTTTGGGAAA	TGACAAAGTT	950
AGAAGCTATA	ATGAAATACA	AAGAATATAT	ACCAGAATAT	ACCTCAGAAC	1000
ATTTTGACAT	GTTAGACGAA	GAAGTTCAAA	GTAGTTTTGA	ATCTGTTCTA	1050
GCTTCTAAGT	CAGATAAATC	AGAAATATTC	TCATCACTTG	GTGATATGGA	1100
GGCATCACCA	CTAGAAAGTTA	AAATTGCATT	TAATAGTAAG	GGTATTATAA	1150
ATCAAGGGCT	AATTTCTGTG	AAAGACTCAT	ATTGTAGCAA	TTTAATAGTA	1200
AAACAAATCG	AGAATAGATA	TAAAAATATTG	AATAATAGTT	TAAATCCAGC	1250
TATTAGCGAG	GATAATGATT	TTAATACTAC	AACGAATACC	TTTATTGATA	1300
GTATAATGGC	TGAAGCTAAT	GCAGATAATG	GTAGATTTAT	GATGGAACATA	1350
GGAAAGTATT	TAAGAGTTGG	TTTCTTCCCA	GATGTAAAAA	CTACTATTAA	1400
CTTAAGTGGC	CCTGAAGCAT	ATGCGGCAGC	TTATCAAGAT	TTATTAATGT	1450
TTAAAGAAGG	CAGTATGAAT	ATCCATTTGA	TAGAAGCTGA	TTTAAGAAAC	1500
TTTGAAATCT	CTAAAACTAA	TATTTCTCAA	TCAACTGAAC	AAGAAATGGC	1550
TAGCTTATGG	TCATTTGACG	ATGCAAGAGC	TAAAGCTCAA	TTTGAAGAAT	1600
ATAAAAGGAA	TTATTTTGAA	GGTTCTCTTG	GTGAAGATGA	TAATCTTGAT	1650
TTTTCTCAAA	ATATAGTAGT	TGACAAGGAG	TATCTTTTAG	AAAAAATATC	1700
TTCATTAGCA	AGAAGTTCAG	AGAGAGGATA	TATACACTAT	ATTGTTTCAGT	1750
TACAAGGAGA	TAAAATTAGT	TATGAAGCAG	CATGTAACCT	ATTTGCAAAG	1800
ACTCCTTATG	ATAGTGTACT	GTTTCAGAAA	AATATAGAAG	ATTCAGAAAT	1850
TGCATATTAT	TATAATCCTG	GAGATGGTGA	AATACAAGAA	ATAGACAAGT	1900
ATAAAATTCC	AAGTATAATT	TCTGATAGAC	CTAAGATTAA	ATTAACATTT	1950
ATTGGTCATG	GTAAAGATGA	ATTTAATACT	GATATATTTG	CAGGTTTTGA	2000
TGTAGATTCA	TTATCCACAG	AAATAGAAGC	AGCAATAGAT	TTAGCTAAAG	2050
AGGATATTTT	TCCTAAGTCA	ATAGAAAATA	ATTTATTAGG	ATGTAATATG	2100
TTTAGCTACT	CTATCAACGT	AGAGGAGACT	TATCCTGGAA	AATTATTACT	2150
TAAAGTTAAA	GATAAAATAT	CAGAATTAAT	GCCATCTATA	AGTCAAGACT	2200
CTATTATAGT	AAGTGCAAAT	CAATATGAAG	TTAGAATAAA	TAGTGAAGGA	2250
AGAAGAGAAT	TATTGGATCA	TTCTGGTGAA	TGGATAAATA	AAGAAGAAAG	2300
TATTATAAAG	GATATTTTCAT	CAAAAGAATA	TATATCATTT	AATCCTAAAG	2350
AAAATAAAAT	TACAGTAAAA	TCTAAAAATT	TACCTGAGCT	ATCTACATTA	2400
TTACAAGAAA	TTAGAAATAA	TTCTAATTCA	AGTGATATTG	AACTAGAAGA	2450
AAAAGTAATG	TTAACAGAAT	GTGAGATAAA	TGTTATTTCA	AATATAGATA	2500
CGCAAATTGT	TGAGGAAAGG	ATTGAAGAAG	CTAAGAATTT	AACTTCTGAC	2550
TCTATTAATT	ATATAAAAGA	TGAATTTAAA	CTAATAGAAT	CTATTTCTGA	2600
TGCACTATGT	GACTTAAAAC	AACAGAATGA	ATTAGAAGAT	TCTCATTTTA	2650
TATCTTTTGA	GGACATATCA	GAGACTGATG	AGGGATTTAG	TATAAGATTT	2700
ATTAATAAAG	AAACTGGAGA	ATCTATATTT	GTAGAACTG	AAAAACAAT	2750
ATTCTCTGAA	TATGCTAATC	ATATAACTGA	AGAGATTTCT	AAGATAAAAG	2800
GTAATAATAT	TGATACTGTA	AATGGTAAGT	TAGTAAAAAA	AGTAAATTTA	2850
GATACTACAC	ACGAAGTAAA	TACTTTAAAT	GCTGCATTTT	TTATACAATC	2900
ATTAATAGAA	TATAATAGTT	CTAAAGAATC	TCTTAGTAAT	TTAAGTGTAG	2950
CAATGAAAGT	CCAAGTTTAC	GCTCAATTAT	TTAGTACTGG	TTTAAATACT	3000
ATTACAGATG	CAGCCAAAGT	TGTTGAATTA	GTATCAACTG	CATTAGATGA	3050
AACTATAGAC	TTACTTCCTA	CATTATCTGA	AGGATTACCT	ATAATTGCAA	3100
CTATTATAGA	TGGTGTAAGT	TTAGGTGCAG	CAATCAAAGA	GCTAAGTGAA	3150
ACGAGTGACC	CATTATTAAG	ACAAGAAATA	GAAGCTAAGA	TAGGTATAAT	3200
GGCAGTAAAT	TTAACAACAG	CTACAACATG	AATCATTACT	TCATCTTTGG	3250
GGATAGCTAG	TGGATTTAGT	ATACTTTTAG	TTCTTTTAGC	AGGAATTTCA	3300
GCAGGTATAC	CAAGCTTAGT	AAACAATGAA	CTTGTAATTC	GAGATAAGGC	3350
AACAAAGGTT	GTAGATTATT	TTAAACATGT	TTTATTAGTT	GAAACTGAAG	3400
GAGTATTTAC	TTTATTAGAT	GATAAAATAA	TGATGCCACA	AGATGATTTA	3450

GTGATATCAG	AAATAGATTT	TAATAATAAT	TCAATAGTTT	TAGGTAAATG	3500
TGAAATCTGG	AGAATGGAAG	GTGGTTCAGG	TCATACTGTA	ACTGATGATA	3550
TAGATCACTT	CTTTTCAGCA	CCATCAATAA	CATATAGAGA	GCCACACTTA	3600
TCTATATATG	ACGTATTGGA	AGTACAAAAA	GAAGAACTTG	ATTTGTCAAA	3650
AGATTTAATG	GTATTACCTA	ATGCTCCAAA	TAGAGTATTT	GCTTGGGAAA	3700
CAGGATGGAC	ACCAGGTTTA	AGAAGCTTAG	AAAATGATGG	CACAAAACCTG	3750
TTAGACCGTA	TAAGAGATAA	CTATGAAGGT	GAGTTTTATT	GGAGATATTT	3800
TGCTTTTATA	GCTGATGCTT	TAATAACAAC	ATTAATAACCA	AGATATGAAG	3850
ATACTAATAT	AAGAATAAAT	TTAGATAGTA	ATACTAGAAG	TTTTATAGTT	3900
CCAATAATAA	CTACAGAATA	TATAAGAGAA	AAATTATCAT	ATTCTTTCTA	3950
TGGTTCAGGA	GGAACCTTATG	CATTGTCTCT	TTCTCAATAT	AATATGGGTA	4000
TAAATATAGA	ATTAAGTGAA	AGTGATGTTT	GGATTATAGA	TGTTGATAAT	4050
GTTGTGAGAG	ATGTAACCTAT	AGAATCTGAT	AAAATTAAAA	AAGGTGATTT	4100
AATAGAAGGT	ATTTTATCTA	CACTAAGTAT	TGAAGAGAAT	AAAATTATCT	4150
TAAATAGCCA	TGAGATTAAT	TTTTCTGGTG	AGGTAAATGG	AAGTAATGGA	4200
TTTGTTTCTT	TAACATTTTC	AATTTTAGAA	GGAATAAATG	CAATTATAGA	4250
AGTTGATTTA	TTATCTAAAT	CATATAAATT	ACTTATTTCT	GGCGAATTAA	4300
AAATATTGAT	GTTAAATTCA	AATCATATTC	AACAGAAAAT	AGATTATATA	4350
GGATTCAATA	GCGAATTACA	GAAAAATATA	CCATATAGCT	TTGTAGATAG	4400
TGAAGGAAAA	GAGAATGGTT	TTATTAATGG	TTCAACAAAA	GAAGGTTTAT	4450
TTGTATCTGA	ATTACCTGAT	GTAGTCTCTA	TAAGTAAGGT	TTATATGGAT	4500
GATAGTAAGC	CTTCATTTGG	ATATTATAGT	AATAATTTGA	AAGATGTCAA	4550
AGTTATAACT	AAAGATAATG	TTAATATATT	AACAGGTTAT	TATCTTAAGG	4600
ATGATATAAA	AATCTCTCTT	TCTTTGACTC	TACAAGATGA	AAAACTATA	4650
AAGTTAAATA	GTGTGCATTT	AGATGAAAGT	GGAGTAGCTG	AGATTTTGAA	4700
GTTTCATGAAT	AGAAAAGGTA	ATACAAATAC	TTCAGATTCT	TTAATGAGCT	4750
TTTTAGAAAG	TATGAATATA	AAAAGTATTT	TCGTTAATTT	CTTACAATCT	4800
AATATTAAGT	TTATATTAGA	TGCTAATTTT	ATAATAAGTG	GTACTACTTC	4850
TATTGGCCAA	TTTGAGTTTA	TTTGTGATGA	AAATGATAAT	ATACAACCAT	4900
ATTTTCATTAA	GTTTAATACA	CTAGAAACTA	ATTATACTTT	ATATGTAGGA	4950
AATAGACAAA	ATATGATAGT	GGAACCAAAT	TATGATTTAG	ATGATTCTGG	5000
AGATATATCT	TCAACTGTTA	TCAATTTCTC	TCAAAAGTAT	CTTTATGGAA	5050
TAGACAGTTG	TGTTAATAAA	GTTGTAATTT	CACCAAATAT	TTATACAGAT	5100
GAAATAAATA	TAACGCCTGT	ATATGAAACA	AATAATACTT	ATCCAGAAGT	5150
TATTGTATTA	GATGCAAATT	ATATAAATGA	AAAAATAAAT	GTTAATATCA	5200
ATGATCTATC	TATACGATAT	GTATGGAGTA	ATGATGGTAA	TGATTTTATT	5250
CTTATGTCAA	CTAGTGAAGA	AAATAAGGTG	TCACAAGTTA	AAATAAGATT	5300
CGTTAATGTT	TTTAAAGATA	AGACTTTGGC	AAATAAGCTA	TCTTTTAACT	5350
TTAGTGATAA	ACAAGATGTA	CCTGTAAGTG	AAATAATCTT	ATCATTTACA	5400
CCTTCATATT	ATGAGGATGG	ATTGATTGGC	TATGATTTGG	GTCTAGTTTC	5450
TTTATATAAT	GAGAAATTTT	ATATTAATAA	CTTTGGAATG	ATGGTATCTG	5500
GATTAATATA	TATTAATGAT	TCATTATATT	ATTTTAAACC	ACCAGTAAAT	5550
AATTTGATAA	CTGGATTGTG	GACTGTAGGC	GATGATAAAT	ACTACTTTAA	5600
TCCAATTAAT	GGTGGAGCTG	CTTCAATTGG	AGAGACAATA	ATTGATGACA	5650
AAAATTATTA	TTTCAACCAA	AGTGGAGTGT	TACAAACAGG	TGTATTTAGT	5700
ACAGAAGATG	GATTTAAATA	TTTTGCCCCA	GCTAATACAC	TTGATGAAAA	5750
CCTAGAAGGA	GAAGCAATTG	ATTTTACTGG	AAAATTAAAT	ATTGACGAAA	5800
ATATTTATTA	TTTTGATGAT	AATTATAGAG	GAGCTGTAGA	ATGGAAAGAA	5850
TTAGATGGTG	AAATGCACTA	TTTTAGCCCA	GAAACAGGTA	AAGCTTTTAA	5900
AGGTCTAAAT	CAAATAGGTG	ATTATAAATA	CTATTTCAAT	TCTGATGGAG	5950
TTATGCAAAA	AGGATTTGTT	AGTATAAATG	ATAATAAACA	CTATTTTGAT	6000
GATTCTGGTG	TTATGAAAGT	AGGTTACACT	GAAATAGATG	GCAAGCATT	6050
CTACTTTGCT	GAAAACGGAG	AAATGCAAAT	AGGAGTATTT	AATACAGAAG	6100
ATGGATTTAA	ATATTTTGCT	CATCATAATG	AAGATTTAGG	AAATGAAGAA	6150
GGTGAAGAAA	TCTCATATTC	TGGTATATTA	AATTTCAATA	ATAAAATTTA	6200
CTATTTTGAT	GATTCATTTA	CAGCTGTAGT	TGGATGGAAA	GATTTAGAGG	6250
ATGGTTCAAA	GTATTATTTT	GATGAAGATA	CAGCAGAAGC	ATATATAGGT	6300

TTGTCATTAA	TAAATGATGG	TCAATATTAT	TTTAATGATG	ATGGAATTAT	6350
GCAAGTTGGA	TTTGTCACTA	TAAATGATAA	AGTCTTCTAC	TTCTCTGACT	6400
CTGGAATTAT	AGAATCTGGA	GTACAAAACA	TAGATGACAA	TTATTTCTAT	6450
ATAGATGATA	ATGGTATAGT	TCAAATTGGT	GTATTTGATA	CTTCAGATGG	6500
ATATAAATAT	TTTGACACCTG	CTAATACTGT	AAATGATAAT	ATTTACGGAC	6550
AAGCAGTTGA	ATATAGTGGT	TTAGTTAGAG	TTGGGGAAGA	TGTATATTAT	6600
TTTGAGAGAA	CATATACAAT	TGAGACTGGA	TGGATATATG	ATATGGAAAA	6650
TGAAAGTGAT	AAATATTATT	TCAATCCAGA	AACTAAAAAA	GCATGCAAAG	6700
GTATTAATTT	AATTGATGAT	ATAAAATATT	ATTTTGATGA	GAAGGGCATA	6750
ATGAGAACGG	GTCTTATATC	ATTTGAAAAT	AATAATTATT	ACTTTAATGA	6800
GAATGGTGAA	ATGCAATTTG	GTTATATAAA	TATAGAAGAT	AAGATGTTCT	6850
ATTTTGGTGA	AGATGGTGTC	ATGCAGATTG	GAGTATTTAA	TACACCAGAT	6900
GGATTTAAAT	ACTTTGCACA	TCAAAATACT	TTGGATGAGA	ATTTTGAGGG	6950
AGAATCAATA	AACTATACTG	GTTGGTTAGA	TTTAGATGAA	AAGAGATATT	7000
ATTTTACAGA	TGAATATATT	GCAGCAACTG	GTTTCAGTTAT	TATTGATGGT	7050
GAGGAGTATT	ATTTTGATCC	TGATACAGCT	CAATTAGTGA	TTAGTGAATA	7100
G					7101

## 2) INFORMATION FOR SEQ ID NO: 2131

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2131

AAGCMATTGT TGTAATTTT GAAAG

25

## 2) INFORMATION FOR SEQ ID NO: 2132

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2132

TCATATCCAT AGCAATAGTT CTA

23

## 2) INFORMATION FOR SEQ ID NO: 2133

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 bases
- (B) TYPE: Nucleic acid

1100



- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2133

CCACGCACAW AAACCTTGTTT TAGAAGTAGC AGCWCAGCGT GG

42

2) INFORMATION FOR SEQ ID NO: 2134

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2134

CGCGTGAAGC TTCTGTG

17

2) INFORMATION FOR SEQ ID NO: 2135

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2135

TCTCGCCGTT ATTCACTTTC

20

2) INFORMATION FOR SEQ ID NO: 2136

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2136

CCAACGCGTC CTCAATCATT TCTAACTTCT ATGGCCGGCG TTGG

44

## 2) INFORMATION FOR SEQ ID NO: 2137

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 889 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas putida*
- (C) ACCESSION NUMBER: Genome project

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2137

ATGATCACCG	GTGCTGCCCA	GATGGACGGC	GCGATCCTGG	TTTGCTCGGC	50
CGCCGATGGT	CCGATGCCrC	AAACCCGTGA	GCACATCCTG	CTGTCCCCTC	100
AGGTAGGCGT	TCCGTACATC	GTGGTCTTCC	TGAACAAGGC	CGACCTGGTA	150
GACGACGCTG	AGCTGCTGGA	ACTGGTCGAG	ATGGAAGTTC	GCGACCTGCT	200
GTCCACCTAC	GACTTCCCAG	GCGACGACAC	TCCGATCATC	ATCGGTTCCT	250
CTCGTATGGC	CCTGGAAGGC	AAAGACGACA	ACGAAATGGG	CACTACCGCT	300
GTCAAGAAGC	TGGTAGAAAC	TCTGGATGCC	TACATCCCTG	AGCCAGTTCT	350
TGCCATCGAC	CAGCCGTTCC	TGATGCCGAT	CGAAGACGTG	TTCTCGATCT	400
CGGGTCGTGG	TACCGTTGTT	ACCGGTCGTA	TGAGCGTGG	CATCGTTCGC	450
GTTTCAGGATC	CGCTGGAAAT	CGTTGGTCTG	CGTGACACCA	CCACCACCAC	500
CTGCACCGGT	GTTGAGATGT	TCCGCAAGCT	GCTGGACGAA	GGTCGTGCTG	550
GCGAGAAGT	GCGCGTTCTG	CTGCGTGGTA	CCAAGCGTGA	CGACGTTGAG	600
CGTGGCCAGG	TTCTGGTCAA	GCCAGGTTCT	GTCAAGCCGC	ACACCAAGTT	650
CACCGCAGAA	GTCTACGTCC	TGTCGAAGGA	AGAAGGCGGC	CGTCACACTC	700
CGTTCTTCAA	AGGCTACCGT	CCACAGTTCT	ACTTCCGTAC	CACTGACGTG	750
ACCGGTAAGT	GCGAACTGCC	GGAAGGCGTT	GAAATGGTAA	TGCCAGGTGA	800
CAACATTGAG	ATGACTGTGA	CCCTGATCAA	GACCATCGCA	ATGGAAGACG	850
GTCTGCGCTT	CGCTATCCGT	GAAGGCGGTC	GTACCGTCG		889

## 2) INFORMATION FOR SEQ ID NO: 2138

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
- (B) STRAIN: PAO-1
- (C) ACCESSION NUMBER: Genome project

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2138

AACATGATCA	CCGGTGCTGC	CCAGATGGAC	GGCGCGATCC	TGGTTTGCTC	50
GGCTGCCGAC	GGCCCCATGC	CGCAGACCCG	CGAGCACATC	CTGCTGTCCC	100
GCCAGGTAGG	CGTTCCCTAC	ATCGTCGTGT	TCCTGAACAA	GGCCGACATG	150
GTCGACGACG	CCGAGCTGCT	GGAAGTGGTC	GAGATGGAAG	TTCGCGATCT	200
GCTGAACACC	TACGACTTCC	CGGGCGACGA	CACTCCGATC	ATCATCGGTT	250
CCGCGCTGAT	GGCGCTGGAA	GGCAAGGATG	ACAACGGCAT	CGGCGTAAGC	300
GCCGTGCAGA	AGCTGGTAGA	GACCCTGGAC	TCCTACATTC	CGGAGCCGGT	350
TCGTGCCATC	GACCAGCCGT	TCCTGATGCC	GATCGAAGAC	GTGTTCTCGA	400
TCTCCGGCCG	CGGTACCGTG	GTAACCGGTC	GTGTAGAGCG	CGGCATCATC	450
AAGGTCCAGG	AAGAAGTGGA	AATCGTCGGC	ATCAAGGCGA	CCACCAAGAC	500
TACCTGCACC	GGCGTTGAAA	TGTTCCGCAA	GCTGCTCGAC	GAAGGTCGTG	550
CTGGTGAGAA	CGTTGGTATC	CTGCTGCGTG	GCACCAAGCG	TGAAGACGTA	600
GAGCGTGGCC	AGGTTCTGGC	CAAGCCGGGC	ACCATCAAGC	CGCACACCAA	650
GTTTCGAGTGC	GAAGTGTACG	TGCTGTCCAA	GGAAGAAGGT	GGTCGTCACA	700
CCCCGTTCTT	CAAGGGCTAC	CGTCCGCACT	TCTACTTCCG	TACCACCGAC	750
GTGACCGGTA	ACTGCGAACT	GCCGGAAGGC	GTAAGATGG	TAATGCCGGG	800
CGACAACATC	AAGATGGTTG	TCACCCTGAT	CGCTCCGATC	GCCATGGAAG	850
ATGGCCTGCG	CTTCGCGATC	CGCGAAGGCG	GCCGTACCGT	TGGCGCCGGC	900

## 2) INFORMATION FOR SEQ ID NO: 2139

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1398 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni*
- (B) STRAIN: NCTC 11168
- (C) ACCESSION NUMBER: AL139074

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2139

ATGCAAGGAT	TTATTTTACA	GGTATTAGGT	CCGGTTGTTG	ATGTAGATTT	50
TAACGACTAT	TTGCCTCAAA	TTAATGAAGC	AATTGTTGTA	AATTTTGAAA	100
GCGAAGGAAA	AAAACATAAA	CTTGTTTTAG	AAGTAGCAGC	TCATTTAGGA	150
GATAATAGAG	TTAGAACTAT	TGCTATGGAT	ATGACAGATG	GTTTGGTAAG	200
GGGCTTAAAA	GCTGAGGCTT	TAGGTGCTCC	CATTAGTGTT	CCTGTTGGTG	250
AGAAAGTTTT	AGGAAGAATT	TTCAATGTTA	CTGGAGATTT	GATCGATGAA	300
GGTGAAGAAA	TTTCTTTTCA	TAAAAAATGG	GCAATTCATA	GAGATCCACC	350
AGCTTTTGAA	GATCAAAGCA	CAAAAAGTGA	GATTTTGTAA	ACAGGGATTA	400
AAGTTGTAGA	TTTACTTGCT	CCTTATGCAA	AAGGTGGTAA	AGTAGGTCTT	450
TTTGGTGGTG	CAGGTGTTGG	TAAAACTGTT	ATTATTATGG	AGCTTATTCA	500
CAATGTTGCA	TTTAAGCATA	GCGGCTATTC	TGTATTTGCA	GGTGTGGGTG	550
AGAGAACTCG	TGAAGGAAAT	GACCTTTATA	ATGAAATGAA	AGAAAGTAAT	600
GTTTTAGACA	AAGTTGCTCT	ATGTTATGGA	CAAATGAATG	AACCACCAGG	650
GGCAAGAAAT	CGTATTGCTT	TAACAGGTTT	AACAATGGCT	GAGTATTTTA	700
GAGATGAAAT	GGGTCTTGAT	GTGCTTATGT	TTATTGATAA	TATCTTTAGA	750
TTTTTACAAT	CAGGTTCTGA	AATGTCAGCA	CTTTTAGGAA	GAATTCCATC	800
AGCTGTGGGT	TATCAACCAA	CCTTAGCAAG	TGAAATGGGT	AAATTCCAAG	850
AAAGAATTAC	TTCAACTAAA	AAAGGCTCAA	TCACTTCAGT	TCAAGCTGTT	900
TACGTTCCAG	CTGATGACTT	AACAGACCCA	GCTCCAGCAA	CTGTTTTTGC	950

TCACCTAGAT	GCTACAACGG	TTTTAAATAG	AGCTATTGCT	GAAAAGGGTA	1000
TTTATCCTGC	AGTTGACCCA	CTTGACTCAA	CTTCAAGAAT	GCTTGACCCA	1050
AATATCATTG	GAGAAGAACA	TTATAAAGTT	GCTCGTGGTG	TTCAATCAGT	1100
GCTTCAAAAA	TACAAAAGATT	TACAAGATAT	CATCGCCATT	TTAGGTATGG	1150
ATGAGCTTAG	CGAAGAGGAT	AAACTTGTAG	TTGAAAGAGC	AAGAAAAGATT	1200
GAAAAATTCT	TATCACAACC	ATTTTTCGTT	GCAGAAGTTT	TCACAGGTAG	1250
CCCAGGAAAA	TATATAAGCC	TTGAAGATAC	AATAGCAGGA	TTTAAGGGAA	1300
TTTTAGAAGG	TAAATATGAT	CATTTACCAG	AAAAATGCTTT	CTATATGGTT	1350
GGAAATATAG	ATGAAGCTAT	TGCAAAAGCG	GATAAATTAA	AAGGTTAA	1398

## 2) INFORMATION FOR SEQ ID NO: 2140

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2157 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: 670
- (C) ACCESSION NUMBER: X67867

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2140

ATGAACAAAC	CAACGATTCT	GCGCCTAATC	AAGTATCTGA	GCATTAGCTT	50
CTTAAGCTTG	GTTATCGCAG	CCATTGTCTT	AGGCGGAGGA	GTTTTTTTCT	100
ACTACGTTAG	CAAGGCTCCT	AGCCTATCCG	AGAGTAAACT	AGTTGCAACA	150
ACTTCTAGTA	AAATCTACGA	CAATAAAAAT	CAACTCATTG	CTGACTTGGG	200
TTCTGAACGC	CGCGTCAATG	CCCAAGCTAA	TGATATTCCC	ACAGATTTGG	250
TTAAGGCAAT	CGTTTCTATC	GAAGACCATC	GCTTCTTCGA	CCACAGGGGG	300
ATTGATTCCA	TCCGTATCCT	GGGAGCTTTC	TTGCGCAATC	TGCAAAAGTAA	350
TTCCCTCCAA	GGTGGATCAA	CTCTCACCCA	ACAGTTGATT	AAGTTGACTT	400
ACTTTTCAAC	CTCGACTTCC	GACCAGACTA	TTTCTCGTAA	GGCTCAGGAA	450
GCTTGGTTAG	CGATTCAATT	AGAACAACAA	GCAACCAAAC	AGGAAATCTT	500
GACCTACTAT	ATAAATAAGG	TCTACATGTC	TAATGGCAAC	TATGGAATGC	550
AGACAGCAGC	TCAAAACTAC	TATGGTAAAG	ACCTCAATAA	TTTAAGTTTA	600
CCTCAGTTAG	CCTTGCTGGC	TGGAATGCCT	CAGGCACCAA	ACCAATATGA	650
CCCCTATTCA	CATCCAGAAG	CAGCCCAAGA	CCGCCGAAAC	TTGGTCTTAT	700
CTGAAATGAA	AAATCAAGGT	TACATCTCTG	CTGAACAGTA	TGAGAAAGCA	750
GTCAATACAC	CAATTACTGA	TGGACTACAA	AGTCTCAAAT	CAGCAAGTAA	800
TTACCCTGCT	TACATGGATA	ATTACCTCAA	GGAGGTCATC	AATCAAGTAG	850
AACAAGAAAC	TGGCTATAAC	CTTCTAACTA	CTGGGATGGA	TGTTTACACA	900
AATGTAGACC	AAGAAGCTCA	AAAACATCTG	TGGGATATCT	ACAACCTCCGA	950
TCAATACGTC	TCTTACCCTG	ACGATGATTT	GCAAGTCGCA	TCTACGGTCG	1000
TAGATGTTTC	AAATGGTAAA	GTCATCGCCC	AACTTGGAGC	TCGTACCCAA	1050
GCAAGTAAAC	TTTCATTGTT	TACCAACCAA	GCTGTGGAAA	CCAATCGTGA	1100
CTGGGGTTCT	GCTATGAAAC	CAATCACCGA	TTATGCACCT	GCCATAGAAT	1150
ACGGTGTTTA	TGATTCCACT	GCAACTATGG	TTAATGATAT	TCCTTATAAC	1200
TATCCGGGAA	CAAGCACACC	TGTCTACAAC	TGGGATAGAG	CATATTTTCGG	1250
TAATATTACT	CTGCAATATG	CTCTTCAACA	ATCACGAAAT	GTCACAGCCG	1300
TTGAGACTTT	GAATAAGGTC	GGTCTAGATA	GAGCTAAAAC	CTTCCTTAAT	1350
GGTCTTGCTA	TCGACTATCC	AAGCATGCAT	TATGCAAACG	CCATTTCAAG	1400

TAATACAACA	GAATCTAATA	AACAATACGG	AGCAAGTAGT	GAAAAAATGG	1450
CTGCTGCTTA	TGCTGCCTTT	GCCAACGGTG	GAATTTACCA	CAAACCCATG	1500
TATATCAATA	AGGTCGTCTT	CAGTGACGGT	AGTAAAAAAG	AATTTTCAGA	1550
TGTAGGTACA	CGAGCTATGA	AAGAAACAAC	TGCTTACATG	ATGACCGAAA	1600
TGATGAAAAC	TGTCTTGGA	TACGGAAGTG	GTCGTGGAGC	CTATCTCCCA	1650
TGGTTAGCGC	AAGCTGGTAA	GACAGGTACT	TCTAACTACA	CAGATGATGA	1700
AATTGAAAAA	CACATCAAGA	AACTGGGCTA	TGTAGCTCCA	GATGAAATGT	1750
TTGTTGGTTA	TACTCGTAAG	TATTCTATGG	CTGTATGGAC	AGGTTATTTCG	1800
AATCGTTTAA	CTCCTATCGT	TGGAGATGGT	TTCCTAGTTG	CAGCTAAAGT	1850
TTATCGCTCA	ATGATAACGT	ATCTATCAGA	AGATACTCAT	CCAGAAGACT	1900
GGACGATGCC	AGACGGACTT	TTCAGAAACG	GGGAATTTGT	ATTCAAAAAT	1950
GGAGCTCGTT	CTACGTGGAG	CTCACCTGCT	CCACAACAAC	CCCCATCAAC	2000
TGAAAGTTCA	AGCTCATCAT	CAGATAGTTC	AACTTCACAG	TCTAGCTCAA	2050
CCACTCCAAG	CACAAATAAT	AGTACGACTA	CCGATCCTAA	CAATAATACG	2100
CAACAATCAA	ATACAACCCC	TGATCAACAA	AATCAGAATC	CTCAACCAGC	2150
ACAACCA					2157

## 2) INFORMATION FOR SEQ ID NO: 2141

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2141

CACCAGTCAC AGAAAAGC

18

## 2) INFORMATION FOR SEQ ID NO: 2142

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2142

GCCTTAATTT CGGATAGTGC

20

## 2) INFORMATION FOR SEQ ID NO: 2143

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1105

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2143

GAGAAAGAGC CCAATTATCT AATGT

25

## 2) INFORMATION FOR SEQ ID NO: 2144

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3075 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: J2870
- (C) ACCESSION NUMBER: X75439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2144

TTGACAAAGA	AATATTTTAA	CACCCAGAAT	GAAATATCAG	CATTTTGGAA	50
TACTCAAAAG	ATATTTTAAA	AATCAATTGA	CAATAGAAAA	GGACAGGAAA	100
GTTTTGTTTT	TTATGACGGC	CCCCCACTG	CAAATGGCCT	TCCTCATGCT	150
GGCCATGTTT	TTGGAAGAGT	AATCAAGGAT	TTAGTTGCAA	GATTAAAAAC	200
TATGCAAGGT	TTTTATGTAG	AAAGAAAAGC	AGGATGGGAT	ACCCATGGCT	250
TACCAGTTGA	ATTAGAGGTT	GAAAAAATAA	TTGGAATTAA	AGGAAAAACA	300
GACATTGAAA	AGTATGGAAT	AGAAAATTTT	ATAAATGAAT	GTAAAAAAG	350
TGTATTTAAT	TATGAAAAAG	AATGGCGGGA	TTTTTCTAAA	GATTTAGGAT	400
ACTGGGTGTA	CATGGACTCC	CCCTATATAA	CTCTTGAGAA	TAATTATATT	450
GAAAGTGAT	GGAATATATT	ATCTACATTC	CATAAAAAAG	GACTATTATA	500
TAAGGGACAT	AAGGTGACTC	CTTATTGTAC	ACATGATCAA	ACCGCTTTAA	550
GTTCTCATGA	AGTAGCGCAA	GGCTATAAAA	ACGTTAAAGA	TTTATCAGCT	600
GTTGTAAAT	TTCAACTTAC	AAATAGTAAA	GATACTTATT	TCTTAAGTTG	650
GACTACCACT	CCCTGGACTT	TGCCTGCAAA	TGTAGCATT	GCTATAAATA	700
AAGATCTTAA	TTATTCAAAA	ATTCGGGTAG	AAAATGAGTA	TTATATCTTA	750
GCTACAGATC	TAATTAATTC	TATAATAACT	GAAAAATACG	AAATTATTGA	800
TACCTTTTCA	GGAAGTAATT	TAATTAATTT	AAAATACATT	CCTCCTTTTG	850
AAAGCGACGG	TTTAGTTAAT	GCATATTACG	TTGTTGATGG	AGAATTTGTT	900
ACTAACTCAG	AAGGAACTGG	TATTGTTTCAT	ATAGCACCAG	CTCATGGGGA	950
AGATGACTAC	CAATTGGTTT	TAGAGCGTGA	TTTGGAATTC	TTAAATGTTA	1000
TAACAAGAGA	AGGAGTATAT	AATGATAGGT	TCCCTGAATT	AGTTGGTAAT	1050
AAAGCTAAAA	ATAGTGATAT	AGAAATCATA	AAATTATTAT	CCAAAAACA	1100
ACTTTTATAT	AAAAAACAAA	AATATGAGCA	TAATTATCCT	CATTGTTGGA	1150
GATGTGGTAA	TCCTTTGATA	TATTATGCGA	TGGAAGGTTG	GTTTATTAAA	1200
ACAATAATT	TTAAGAATGA	AATTATTAAC	AATAATAATA	ATATAGAGTG	1250
GTTTCCTTCT	CATATTAAGG	AAGGGAGAAT	GGGAAATTTT	TTAGAAAATA	1300
TGGTTGATTG	GAACATTGGT	AGAAATAGAT	ATTGGGGAAC	ACCATTAAAT	1350
GTATGGATTT	GCAATGATTG	TAATCACGAA	TACGCACCAA	GTAGTATTAA	1400
GGATTTACAA	AATAATTCCA	TCAATAAAAT	TGATGAAGAT	ATTGAGTTGC	1450
ATAGACCTTA	TGTTGATAAT	ATCACTCTTA	GTTGCCCTAA	GTGTAATGGG	1500

1106

AAAATGTCTC	GAGTAGAAGA	AGTAATCGAT	GTTTGGTTTG	ATAGCGGCTC	1550
TATGCCGTTT	GCTCAGCATC	ATTATCCTTT	TGATAACCAG	AAAATTTTAA	1600
ATCAACACTT	TCCAGCTGAT	TTTATTGCAG	AAGGAGTTGA	TCAAACGAGA	1650
GGCTGGTTTT	ACAGTTTACT	AGTAATTTCT	ACTATTCTAA	AAGGAAAATC	1700
TTCTTATAAA	CGTGCTTTAT	CTTTAGGACA	TATTCTAGAC	AGTAATGGTA	1750
AAAAAATGTC	TAAAAGTAAA	GGAAACGTTA	TTAATCCAAC	TGAATTAATT	1800
AATAAGTACG	GAGCCGATTC	TTTAAGATGG	GCCTTAATTT	CGGATAGTGC	1850
TCCATGGAAT	AACAAAAGAT	TCTCAGAAAA	TATAGTAGCT	CAGACCAAAT	1900
CGAAATTTAT	AGATACGCTT	GATAATATTT	ATAAATTTTA	TAATATGTAT	1950
AATAAAATAG	ATCACTATAA	TCCTAATAAT	GAAATTACAA	AAAGTAGAAA	2000
TACATTAGAT	AATTGGGCTC	TTTCTCGCTT	AAACACCTTA	ATAAAAGAAA	2050
GTAATATTTA	TGTAATAAAT	TACGATTTCA	CTTCCGCAGC	CAGATTAATT	2100
AACGAATATA	CCAATACAAT	AAGTAATTGG	TATATCGGAG	ATTCGAGAGG	2150
ACGATTTTGG	GAACAAGGAA	TTTCTAACGA	TAAAAAAGAT	GCGTACAATA	2200
CGCTTTATGA	AATTTTAACA	ACTTTATCAA	GACTAGTGGC	TCCATTTGTT	2250
CCATTTATAT	CTGAAAAAAT	CCATTATAAT	TTGACTGGAA	AAAGTGTGCA	2300
TTTACAAGAT	TATCCACAAT	ATAAAGAAAG	TTTTATTAAT	CAAGCATTGG	2350
AAGATGAAAT	GCATACCGTT	ATAAAAATTG	TAGAATTATC	TAGACAGGCT	2400
CGCAAAAATG	CAGATTTAAA	AATTAAGCAA	CCTTTATCGA	AAATGGTGAT	2450
TAAACCTAAT	AGTCAATTAA	ACTTAAGTTT	TTTACCTAAT	TACTATTCAA	2500
TAATAAAAGA	CGAATTAAAT	ATAAAAAACA	TTGAATTAAC	TGATAATATT	2550
AATGACTATA	TTACCTATGA	GCTTAAATTG	AATTTTTCTT	CTGTGGGACC	2600
AAAAC TAGGG	AACAAAACGA	AAAATATTCA	AACATTGATA	GACTCCCTAT	2650
CAGAGTATGA	TAAAAAAAGT	TTAATTGAGT	CTAATAACTT	CAAAAGTTTA	2700
TCTTCTGATG	CTGAGTTAAC	TAAGGATGAT	TTTATAATTA	AAACCTTACC	2750
TAAGGATAGT	TATCAACTCA	GTGAAGATAA	TGACTGCGTT	ATATTATTAG	2800
ATAAAAATTT	ATCTCCTGAA	TTAATTGCGG	AAGGACATGC	TAGAGAGCTC	2850
ATTAGATTAA	TTCAACAATT	AAGAAAAAAG	AAAAATTTAC	CAATAAATCA	2900
ACGTATTGAT	ATTTATATCG	GTGTAAC TGG	GGAATTATTA	GAATCAATAA	2950
AAACCAATAA	AAATATGTTT	AAAGAAAATT	TCGTGATTAA	AAATATACAC	3000
TTAAATGTTA	TAGATGAATA	TGAAAATACT	ATTCATTTTA	ATAATAAAGA	3050
AATAAAAATT	TCCTTATTAT	ATTAA			3075

## 2) INFORMATION FOR SEQ ID NO: 2145

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2145

GCAAGATGTG GCGTGTTACG GT

22

## 2) INFORMATION FOR SEQ ID NO: 2146

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1107

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2146

GGGGCGAAGA AGTTGTCCAT ATT

23

## 2) INFORMATION FOR SEQ ID NO: 2147

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: V00622

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2147

ATGGAGAAAA	AAATCACTGG	ATATACCACC	GTTGATATAT	CCCAATGGCA	50
TCGTAAAGAA	CATTTTGAGG	CATTTCAGTC	AGTTGCTCAA	TGTACCTATA	100
ACCAGACCGT	TCAGCTGGAT	ATTACGGCCT	TTTTAAAGAC	CGTAAAGAAA	150
AATAAGCACA	AGTTTATCC	GGCCTTTATT	CACATTCTTG	CCCGCCTGAT	200
GAATGCTCAT	CCGGAATTCC	GTATGGCAAT	GAAAGACGGT	GAGCTGGTGA	250
TATGGGATAG	TGTTACCCCT	TGTTACACCG	TTTTCCATGA	GCAAACCTGAA	300
ACGTTTTTCAT	CGCTCTGGAG	TGAATACCAC	GACGATTTCC	GGCAGTTTCT	350
ACACATATAT	TCGCAAGATG	TGGCGTGTTA	CGGTGAAAAC	CTGGCCTATT	400
TCCCTAAAGG	GTTTATTGAG	AATATGTTTT	TCGTCTCAGC	CAATCCCTGG	450
GTGAGTTTCA	CCAGTTTGA	TTTAAACGTG	GCCAATATGG	ACAACTTCTT	500
CGCCCCCGTT	TTCACCATGG	GCAAATATTA	TACGCAAGGC	GACAAGGTGC	550
TGATGCCGCT	GGCGATTCAG	GTTTCATCATG	CCGTCTGTGA	TGGCTTCCAT	600
GTCGGCAGAA	TGCTTAATGA	ATTACAACAG	TACTGCGATG	AGTGGCAGGG	650
CGGGGCGTAA					660

## 2) INFORMATION FOR SEQ ID NO: 2148

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2148

CAGATTAAAT GCGGATTCAG CC

22



## 2) INFORMATION FOR SEQ ID NO: 2149

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2149

ATCAGGTAAA TCATCAGCGG ATA

23

## 2) INFORMATION FOR SEQ ID NO: 2150

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: K12
- (C) ACCESSION NUMBER: X53796

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2150

ATGAATTTTA	CCCGGATTGA	CCTGAATACC	TGGAATCGCA	GGAACACTT	50
TGCCCTTTAT	CGTCAGCAGA	TTAAATGCGG	ATTCAGCCTG	ACCACCAAAC	100
TCGATATTAC	CGCTTTGCGT	ACCGCACTGG	CGGAGACAGG	TTATAAGTTT	150
TATCCGCTGA	TGATTTACCT	GATCTCCCGG	GCTGTTAATC	AGTTTCCGGA	200
GTTCCGGATG	GCACTGAAAG	ACAATGAACT	TATTTACTGG	GACCAGTCAG	250
ACCCGGTCTT	TACTGTCTTT	CATAAAGAAA	CCGAAACATT	CTCTGCACTG	300
TCCTGCCGTT	ATTTTCCGGA	TCTCAGTGAG	TTTATGGCAG	GTTATAATGC	350
GGTAACGGCA	GAATATCAGC	ATGATACCAG	ATTGTTTCCG	CAGGGAAATT	400
TACCGGAGAA	TCACCTGAAT	ATATCATCAT	TACCGTGGGT	GAGTTTTGAC	450
GGATTTAACC	TGAACATCAC	CGGAAATGAT	GATTATTTTG	CCCCGGTTTT	500
TACGATGGCA	AAGTTTCAGC	AGGAAGGTGA	CCGCGTATTA	TTACCTGTTT	550
CTGTACAGGT	TCATCATGCA	GTATGTGATG	GCTTTCATGC	AGCACGGTTT	600
ATTAATACAC	TTCAGCTGAT	GTGTGATAAC	ATACTGAAAT	AA	642

## 2) INFORMATION FOR SEQ ID NO: 2151

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid

1109

- (C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2151

ATATTTCAGC ATTACCTTGG GTT

23

## 2) INFORMATION FOR SEQ ID NO: 2152

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2152

TACACAAC TC TTGTAGCCGA TTA

23

## 2) INFORMATION FOR SEQ ID NO: 2153

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 642 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella flexneri*  
(C) ACCESSION NUMBER: X07848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2153

ATGAACTATA	CAAAATTTGA	TGTAAAAAAT	TGGGTTTCGCC	GTGAGCATTT	50
TGAGTTTTAT	CGGCATCGTT	TACCATGTGG	TTTATAGCTTA	ACAAGCAAAA	100
TTGATATCAC	GACGTTAAAA	AAGTCATTGG	ATGATTCAGC	GTATAAGTTT	150
TATCCGGTAA	TGATCTATCT	GATTGCTCAG	GCCGTGAATC	AATTTGATGA	200
GTTGAGAATG	GCGATAAAAG	ATGATGAATT	GATCGTATGG	GATTCAGTCG	250
ACCCACAATT	CACCGTATTC	CATCAAGAAA	CAGAGACATT	TTCAGCACTG	300
AGTTGCCCAT	ACTCATCCGA	TATTGATCAA	TTTATGGTGA	ATTATTTATC	350
GGTAATGGAA	CGTTATAAAA	GTGATACCAA	GTTATTTTCCT	CAAGGGGTAA	400
CACCAGAAAA	TCATTTAAAT	ATTTTCAGCAT	TACCTTGGGT	TAATTTTGAT	450
AGCTTTAATT	TAAATGTTGC	TAATTTTACC	GATTATTTTG	CACCCATTAT	500
AACAATGGCA	AAATATCAGC	AAGAAGGGGA	TAGACTGTTA	TTGCCGCTCT	550
CAGTACAGGT	TCATCATGCA	GTTTGTGATG	GCTTCCATGT	TGCACGCTTT	600
ATTAATCGGC	TACAAGAGTT	GTGTAACAGT	AAATTAAAAT	AA	642

## 2) INFORMATION FOR SEQ ID NO: 2154

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2154

CGCCATTCAG AGTTTAGGAC

20

## 2) INFORMATION FOR SEQ ID NO: 2155

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2155

TTCCATACCG TTGCGTATCA CTT

23

## 2) INFORMATION FOR SEQ ID NO: 2156

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium perfringens*
- (B) STRAIN: CP590
- (C) ACCESSION NUMBER: M74769

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2156

ATGGTATTTG	AAAAAATTGA	TAAAAATAGT	TGGAACAGAA	AAGAGTATTT	50
TGACCACTAC	TTTGCAAGTG	TACCTTGATC	ATACAGCATG	ACCGTTAAAG	100
TGGATATCAC	ACAAATAAAG	GAAAAGGGAA	TGAAACTATA	TCCTGCAATG	150
CTTTATTATA	TTGCAATGAT	TGTAAACCGC	CATTGAGAGT	TTAGGACGGC	200
AATCAATCAA	GATGGTGAAT	TGGGGATATA	TGATGAGATG	ATACCAAGCT	250

1111

ATACAATATT	TCACAATGAT	ACTGAAACAT	TTTCCAGCCT	TTGGACTGAG	300
TGTAAGTCTG	ACTTTAAATC	ATTTTATGCA	GATTATGAAA	GTGATACGCA	350
ACGGTATGGA	AACAATCATA	GAATGGAAGG	AAAGCCAAAT	GCTCCGGAAA	400
ACATTTTAA	TGTATCTATG	ATACCGTGGT	CAACCTTCGA	TGGCTTTAAT	450
CTGAATTTGC	AGAAAGGATA	TGATTATTTG	ATTCCCTATT	TTACTATGGG	500
GAAATATTAT	AAAGAAGATA	ACAAAATTAT	ACTTCCTTTG	GCAATTCAAG	550
TTCATCACGC	AGTATGTGAC	GGATTTTACA	TTTGCCGTTT	TGTAAACGAA	600
TTGCAGGAAT	TGATAAATAG	TTAA			624

## 2) INFORMATION FOR SEQ ID NO: 2157

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2157

CCACAGAAAT TGATATTAGT GTTTTAT

27

## 2) INFORMATION FOR SEQ ID NO: 2158

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2158

TCGCTATTGT AACCAGTTCT A

21

## 2) INFORMATION FOR SEQ ID NO: 2159

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (C) ACCESSION NUMBER: V01277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2159

ATGAACTTTA	ATAAAATTGA	TTTAGACAAT	TGGAAGAGAA	AAGAGATATT	50
TAATCATTAT	TTGAACCAAC	AAACGACTTT	TAGTATAACC	ACAGAAATTG	100
ATATTAGTGT	TTTATACCGA	AACATAAAAC	AAGAAGGATA	TAAATTTTAC	150
CCTGCATTTA	TTTTCTTAGT	GACAAGGGTG	ATAAACTCAA	ATACAGCTTT	200
TAGAACTGGT	TACAATAGCG	ACGGAGAGTT	AGGTTATTGG	GATAAGTTAG	250
AGCCACTTTA	TACAATTTTT	GATGGTGTAT	CTAAAACATT	CTCTGGTATT	300
TGGACTCCTG	TAAAGAATGA	CTTCAAAGAG	TTTTATGATT	TATACCTTTC	350
TGATGTAGAG	AAATATAATG	GTTTCGGGGA	ATTGTTTCCC	AAAACACCTA	400
TACCTGAAAA	TGCTTTTTCT	CTTTCTATTA	TTCCATGGAC	TTCATTTACT	450
GGGTTTAACT	TAAATATCAA	TAATAATAGT	AATTACCTTC	TACCCATTAT	500
TACAGCAGGA	AAATTCATTA	ATAAAGGTAA	TTCAATATAT	TTACCGCTAT	550
CTTTACAGGT	ACATCATTCT	GTTTGTGATG	GTTATCATGC	AGGATTGTTT	600
ATGAACTCTA	TTCAGGAATT	GTCAGATAGG	CCTAATGACT	GGCTTTTATA	650
A					651

2) INFORMATION FOR SEQ ID NO: 2160

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2160

TTTTGAACAC TATTTTAACC AGC

23

2) INFORMATION FOR SEQ ID NO: 2161

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2161

GATTTAACTT ATCCCAATAA CCT

23

2) INFORMATION FOR SEQ ID NO: 2162

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

1113

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(C) ACCESSION NUMBER: X02166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2162

ATGACTTTTA	ATATTATCAA	ATTAGAAAAT	TGGGATAGAA	AAGAATATTT	50
TGAACACTAT	TTTAACCAGC	AAACTACGTA	TAGCATTACT	AAAGAAATTG	100
ATATTACTTT	GTTTAAAGAT	ATGATAAAAA	AGAAAGGATA	TGAAATTTAT	150
CCTTCTTTGA	TTTATGCAAT	TATGGAAGTT	GTAAATAAAA	ATAAAGTGTT	200
TAGAACAGGA	ATTAATAGTG	AGAATAAATT	AGGTTATTGG	GATAAGTTAA	250
ATCCTTTGTA	TACAGTTTTT	AATAAGCAAA	CTGAAAAATT	TACTAACATT	300
TGGACTGAAT	CTGATAACAA	CTTCACTTCT	TTTTATAATA	ATTATAAAAA	350
TGACTTGCTT	GAATATAAAG	ATAAAGAAGA	AATGTTTCCT	AAAAAACCGA	400
TACCTGAAAA	CACCATACCG	ATTTCAATGA	TTCCTTGGAT	TGATTTTAGT	450
TCATTTAATT	TAAACATTGG	TAACAATAGC	AACTTTTAT	TGCCTATTAT	500
TACGATAGGT	AAATTTTATA	GTGAGAATAA	TAAAATTTAT	ATACCAGTTG	550
CTTTGCAGCT	TCATCATGCT	GTATGTGATG	GTTACCATGC	TTCATTATTT	600
ATGAATGAAT	TTCAAGATAT	AATTCATAAG	GTAGATGATT	GGATTTAG	648

2) INFORMATION FOR SEQ ID NO: 2163

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2163

ACCTTCATCC TACCGATGTG GGTT

24

2) INFORMATION FOR SEQ ID NO: 2164

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2164

CAACGACACC AGCACTGCCA TTG

23

2) INFORMATION FOR SEQ ID NO: 2165

1114

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1215 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella typhimurium*
- (B) STRAIN: H3380
- (C) ACCESSION NUMBER: AF071555

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2165

ATGACCACCA	CACGCCCCGC	GTGGGCCTAT	ACGCTGCCGG	CAGCACTGCT	50
GCTGATGGCT	CCTTTCGACA	TCCTCGCTTC	ACTGGCGATG	GATATTTATC	100
TCCCTGTCGT	TCCAGCGATG	CCCGGCATCC	TGAACACGAC	GCCCGCTATG	150
ATCCAACTCA	CGTTGAGCCT	CTATATGGTG	ATGCTCGGCG	TGGGCCAAGT	200
GATTTTTTGGT	CCGCTCTCAG	ACAGAATCGG	GCGACGGCCA	ATTCTACTTG	250
CGGGCGCAAC	GGCTTTCGTC	ATTGCGTCTC	TGGGAGCAGC	TTGGTCTTCA	300
ACTGCACCGG	CCTTTGTGCG	TTTCCGTCTA	CTTCAAGCAG	TGGGCGCGTC	350
GGCCATGCTG	GTGGCGACGT	TCGCGACGGT	TCGCGACGTT	TATGCCAACC	400
GTCCTGAGGG	TGTCGTCATC	TACGGCCTTT	TCAGTTCGAT	GCTGGCGTTC	450
GTGCCTGCGC	TCGGCCCTAT	CGCCGGAGCA	TTGATCGGCG	AGTTCTTGGG	500
ATGGCAGGCG	ATATTCATTA	CTTTGGCTAT	ACTGGCGATG	CTCGCACTCC	550
TAAATGCGGG	TTTCAGGTGG	CACGAAACCC	GCCCTCTGGA	TCAAGTCAAG	600
ACGCGCCGAT	CTGTCTTGCC	GATCTTCGCG	AGTCCGGCTT	TTTGGGTTTA	650
CACTGTCGGC	TTTAGCGCCG	GTATGGGCAC	CTTCTTCGTC	TTCTTCTCGA	700
CGGCTCCCCG	TGTGCTCATA	GGCCAAGCGG	AATATTCCGA	GATCGGATTC	750
AGCTTTGCCT	TCGCCACTGT	CGCGCTTGTA	ATGATCGTGA	CAACCCGTTT	800
CGCGAAGTCC	TTTGTGCTCA	GATGGGGCAT	CGCAGGATGC	GTGGCGCGTG	850
GGATGGCGTT	GCTTGTTTGC	GGAGCGGTCC	TGTTGGGGAT	CGGCGAACTT	900
TACGGCTCGC	CGTCATTCCT	CACCTTCATC	CTACCGATGT	GGGTGTGTCG	950
GGTCGGTATT	GTCTTCACGG	TGTCCGTTAC	CGCGAACGGC	GCTTTGGCAG	1000
AGTTCGACGA	CATCGCGGGA	TCAGCGGTGC	CGTTCTACTT	CTGCATCCAA	1050
AGCCTGATAG	TCAGTATCGT	CGGGACATTG	GCGGTGACGC	TGTTAAACGG	1100
CGATACAGCG	TGGCCCGTGA	TTTGTTACGC	CACGGCAATG	GCAGTGCTGG	1150
TGTCGTTGGG	GCTGGCGCTC	CTTCGATCCC	GTGATGCTGC	CACCGAGAAG	1200
TCGCCAGTCG	TCTAG				1215

## 2) INFORMATION FOR SEQ ID NO: 2166

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2166

GACAAACCAT TCCTGCTG

## 2) INFORMATION FOR SEQ ID NO: 2167

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2167

CAGCAGCTGG GCGGCGGT

18

## 2) INFORMATION FOR SEQ ID NO: 2168

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2168

CATCAAAGTT GGTGAAGAAG TTG

23

## 2) INFORMATION FOR SEQ ID NO: 2169

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2169

CCCGTTTGCG AAAGGTGG

18

## 2) INFORMATION FOR SEQ ID NO: 2170

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1116



(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2170

ACGTGACGTT GACAAACCA

19

2) INFORMATION FOR SEQ ID NO: 2171

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2171

TCGTTGGATT AACTGAAGAA

20

2) INFORMATION FOR SEQ ID NO: 2172

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2172

GTGTTGAAAT GTTCCGTAAA

20

2) INFORMATION FOR SEQ ID NO: 2173

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2173

AAGAAAAAAT CTTCGAACTG GCTA

24

2) INFORMATION FOR SEQ ID NO: 2174

1117

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2174

TCTACACGGC CGGTG

15

## 2) INFORMATION FOR SEQ ID NO: 2175

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2175

CCGCCATACC CCGTTT

16

## 2) INFORMATION FOR SEQ ID NO: 2176

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2176

CGGCATTACC ATTTCCACAC CTTT

24

## 2) INFORMATION FOR SEQ ID NO: 2177

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2177

GGCACGGACA AACCATTCTT GCTGCCTATC GAAGACGTGT TCCCGTGCC 49

2) INFORMATION FOR SEQ ID NO: 2178

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2178

GGCACGACAA ACCATTCTTG CTGCCTATCG AACGTGCC 38

2) INFORMATION FOR SEQ ID NO: 2179

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2179

GGCAGCTCTA CTTCCGTACC ACTGACGTAA CCGGCTGCC 39

2) INFORMATION FOR SEQ ID NO: 2180

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2180

TTCGCCGGCG TGGGC 15

2) INFORMATION FOR SEQ ID NO: 2181

(i) SEQUENCE CHARACTERISTICS:

1119

- (A) LENGTH: 15 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2181

AGCGCCACGC GCAGG

15

## 2) INFORMATION FOR SEQ ID NO: 2182

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2182

GCGCGCCAAC GACTTCTACC ACGAAATGGA AGAGTCGCGC GC

42

## 2) INFORMATION FOR SEQ ID NO: 2183

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Alcaligenes faecalis* subsp. *faecalis*
- (B) STRAIN: ATCC 8750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2183

TATCTTGGTT	WGCTCGGCCG	CTGACGGCCC	AATGCCTCAG	ACTCGCGAGC	50
ACATCCTGCT	GAGCCGTCAG	GTTGGCGTTC	CTTACATCAT	CGTGTTTCCTG	100
AACAAGGCCG	ACATGGTTGA	TGACGAAGAG	CTGATCGAAC	TGGTTGAAAT	150
GGAAGTTCGC	GAGCTGTTGT	CCAAGTACGA	CTTCCCTGGC	GACGACACCC	200
CGATCATCAA	GGGTTCGGCC	AAACTGGCTC	TGGAAGGCCA	CGAAGGCCCA	250
CTGGGCAGCC	AAGCCGTTCT	GGCTCTGGCC	GAAGCGCTGG	ACAACTACAT	300
TCCTACGCCT	GAGCGTGCCG	TTGACGGTAC	GTTCCCTGATG	CCTGTTGAAG	350
ACGTGTTCTC	GATCTCCGGC	CGTGGTACGG	TTGTGACCGG	TCGTATTGAG	400
CGCGGCATCA	TCAAGGTCGG	CGAAGAAATC	GAAATCGTGG	GTATCAAAGA	450
CACGGTCAAG	ACCATTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
ACCAGGGCGA	AGCTGGCGAT	AACGTCGGTC	TGCTGCTGCG	TGGTACCAAG	550
CGTGAAGACG	TGGAACGTGG	TCAAGTTCTG	GCCAAGCCAG	GCTCGATCAA	600
GCCACACACT	GACTTCGACG	CCGAGGTGTA	CATTCTGTCC	AAAGAAGAAG	650
GTGGTCGTCA	CACTCCTTTC	TTCAAGGGCT	ACCGTCCTCA	GTTCTACTTC	700

CGTACAAC	TCG	ACGTGACCGG	CACCATCGAG	CTGCCAGAAG	ACAAGGAAAT	750
GGTTCTGCCA	GGCGACAACA	TTTCGATGAA	AGTGTCCCTG	ATCGCTCCTA		800
TCGCCATGGA	AGAAGGT					817

## 2) INFORMATION FOR SEQ ID NO: 2184

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1652 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter coli*
- (B) STRAIN: ATCC 43479

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2184

TACAATTGAA	GTTGAAAGAT	CTATGCGTGT	TCTTGATGGT	GCTGTTGCGG	50
TATTTTGTTC	AGTGGGTGGG	GTGCAGCCTC	AAAGTGAAAC	AGTTTGGAGA	100
CAAGCAAATA	AATATGGTGT	TCCAAGAATA	GTATTTGTAA	ATAAAATGGA	150
TAGAATCGGT	GCAAATTTCT	ACAATGTAGA	AGATCAAATT	CGCAACCGTT	200
TAAAAGCTAA	TCCAGTTCCA	CTTCAAATTC	CAATCGGTGC	TGAGGATAAT	250
TTTAAAGGCG	TAATCGATCT	TGTAACATG	AAAGCTTTAG	TTTGGGAAGA	300
TGATACTAAG	CCAACGGATT	ATGTAGAAAA	AGAAATTCCA	GCTGAACTTA	350
AAGAAAAGGC	AGAAGAATAT	CGCACAAAAA	TGATAGAAGC	AGTTTCTGAA	400
ACTTCAGATG	AGTTGATGGA	AAAATATTTA	GGTGGAGAAG	AATTAAGCCT	450
TGAAGAGATT	AAAACAGGGA	TTAAAGCAGG	ATGTTTAAGT	CTTCTATCG	500
TTCTATGCT	TTGCGGTACA	GCGTTTAAAA	ATAAAGGGGT	TCAACCTTTG	550
CTTGATGCTG	TTGTGGCTTA	TTTACCAGCT	CCTGATGAAG	TTGCTAATAT	600
CAAAGGGGAA	TATGAAGACG	GCACAGAAGT	TTCTGTAAAA	TCAACTGATG	650
ATGGCGAATT	TGCAGGACTT	GCATTTAAAA	TTATGACAGA	TCCATTTGTA	700
GGACAACCTA	CTTTCGTGCG	TGTTTATCGT	GGATGTTTAG	AAAGCGGTTT	750
TTATGCTTAT	AACTCAACCA	AAGATAAAAA	AGAAAGAATT	GGTCGTTTGT	800
TAAAAATGCA	CTCTAATAAA	AGAGAAGAAA	TTAAAGTTCT	TTACGCAGGA	850
GAAATCGGTG	CAGTTGTAGG	ACTTAAAGAT	ACTTTAACAG	GGGATACTCT	900
TGCAAGTGAA	AAAGATAAAG	TAATTCTTGA	AAGAATGGAT	TTCCCAGACC	950
CAGTTATTTT	TGTTGCAGTA	GAMCCAAAAA	CTAAAGCAGA	TCAAGAAAAA	1000
ATGTCTATTG	CACTAAATAA	ATTAGCTCAA	GAAGATCCAA	GCTTTAGAGT	1050
TTCTACGGAT	GAAGAAAGTG	GTCAAACAT	CATTTACAGT	ATGGGTGAAT	1100
TACACCTTGA	AATTATTGTT	GATCGTATGC	TTCTGTGAAT	TAAAGTGGAA	1150
GCTGAAGTGG	GACAACCTCA	AGTTGCTTAT	CGTGAAACTA	TCAGAAAAAC	1200
TGTTGAGCAA	GAATACAAAT	ACGCTAAGCA	ATCAGGCGGT	CGTGGTCAGT	1250
ATGGACATGT	ATTCTTACGC	CTTGAGCCAC	TTGAGCCAGG	AAGTGGATAC	1300
GAGTTTGTTA	ACGACATCAA	AGGTGGGGTA	ATTCCAAAAG	AATATATTCC	1350
TGCAGTAGAT	AAGGGTGTTT	AAGAAGCATT	GCAAAATGGT	GTTTTAGCAG	1400
GTTATCCAGT	AGAAGATGTT	AAAGTAACTG	TTTATGATGG	AAGTTATCAC	1450
GAGGTGGATT	CATCTGAGAT	GGCATTTAAA	CTTGCTGCTT	CTATGGGATT	1500
TAAAGAGGGT	GCTAGAAAAG	CAGGTGCTGT	GATCTTAGAG	CCTATGATGA	1550
AAGTTGAAGT	AGAACTCCT	GAAGATTACA	TGGGCGATGT	TATTGGCGAT	1600
CTTAATAAGC	GTCGTGGTCA	AGTAAATAGC	ATGGATGAAA	GAGGTGGTAA	1650
TA					1652

## 2) INFORMATION FOR SEQ ID NO: 2185

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Succinivibrio dextrinosolvens*
- (B) STRAIN: ATCC 19716

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2185

GCTATTCTAG	TAGTAGCAGC	AACTGATGGT	CCTATGCCAC	AGACCCGTGA	50
GCACATCCTA	TTAGCACGTC	AGGTAGGCGT	ACCATACATC	ATCGTATTCC	100
TAAACAAGTG	CGATATGGTT	GACGACGAGG	AATTATTAGA	GTTAGTTGAG	150
ATGGACGTAC	GTGATCTATT	AAATCAGTAC	CAGTTCCCAG	GCGACGACAC	200
TCCAATCATC	CGTGGTTCAG	CACTAGGTGC	ATTAAACGGC	GAAGAGAAGT	250
GGAAAGAGGC	AATCTATCAG	TTAGCAGACA	CTCTAGATTG	ATACATTCCA	300
GAGCCAAAGC	GTGATATCGA	TGATCCATTG	CTATTACCAA	TCGAAGATAT	350
CTTCTCAATC	TCAGGTCGTG	GTACTGTAGT	AACCGGCCGT	GTAGAGCGTG	400
GTATTGTACA	CGTAGGTGAC	GAAGTTGAAA	TCGTTGGTAT	TCGTCCAACC	450
ACCAAGACCA	CTGTAAGTGG	CGTTGAAATG	TTCCGTAAGT	TACTAGACGA	500
AGGTCGTGCA	GGTGATAACG	TTGGTGTTCT	ACTACGTGGT	ACCAAGCGTG	550
ATGAGGTTGA	GCGTGGTCAG	GTTCTAGCTG	CTCCAGGCAC	AATCACTCCA	600
CACACCAAGT	TCACTGGTCA	GGTTTACGTA	CTAAGCAAGG	ATGAAGGTGG	650
TCGTCACACT	CCATTCTTCA	AGGGCTACCG	TCCACAGTTC	TTCTTCCGTA	700
CAACCGATAT	TACCGGTTCT	ATCGATCTGA	AAGAGGGCGT	AGAGATGGTA	750
ATGCCAGGTG	ATAACACCGA	CATGACCGTA	ACCCTAATCC	ACCCAGTAGC	800
TATGGCTGAA	GGCGAGAGAT				820

## 2) INFORMATION FOR SEQ ID NO: 2186

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2186

ACGCGCTCAA AGCAGAAGTA TACGTATTAT CAAAAGACGC GCGT

44

## 2) INFORMATION FOR SEQ ID NO: 2187

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1612 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni* subsp. *jejuni*
- (B) STRAIN: ATCC 33292

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2187

```

CAGTGGGTGG GGTGCAGCCT CAAAGTGAAA CAGTTTGGAG ACAAGCAAAT      50
AAATATGGTG TTCCAAGAAT AGTATTTGTA AACAAAATGG ATAGAATCGG      100
TGCAAATTTTC TACAATGTAG AAGATCAAAT TCGCAACCGT TTAAAAGCTA      150
ATCCAGTTCC ACTTCAAATT CCAATCGGTG CTGAGGATAA TTTTAAAGGC      200
GTAATCGATC TTGTAACAT GAAAGCTTTA GTTTGGGAAG ATGATACTAA      250
GCCAACGGAT TATGTAGAAA AAGAAATTCC AGCTGAACTT AAAGAAAAGG      300
CAGAAGAATA TCGCACAAAA ATGATAGAAG CAGTTTCTGA AACTTCAGAT      350
GAGTTGATGG AAAAATATTT AGGCGGAGAA GAATTAAGCC TTGAAGAGAT      400
TAAAACAGGG ATTAAAGCAG GATGTTTAAG TCTTTCTATC GTTCCTATGC      450
TTTGCGGTAC AGCGTTTAAA AATAAAGGGG TTCAACCTTT ACTTGATGCT      500
GTTGTGGCTT ATTTACCAGC TCCTGATGAA GTGGCAAATA TCAAGGGTGA      550
ATATGAAGAT GGCACAGAAG TTTCTGTAAA ATCAACTGAT GATGGCGAGT      600
TTGCAGGACT TGCATTTAAA ATTATGACAG ATCCATTTGT AGGACAACCT      650
ACTTTCGTGC GTGTTTATCG CGGTGTTTAA GAAAGTGGTT CTTATGCTTA      700
TAACTCAACT AAAGATAAAA AAGAAAGAAT TGGTCGTTTG TTAAAAATGC      750
ACTCTAACCA AAGAGAAGAG ATTAAAGTGC TTTACGCAGG CGAAATTGGT      800
GCTGTTGTAG GACTTAAAGA TACTTTAACA GGGGATACTC TTGTAAGTGA      850
AAAAGATAAG GTAATCCTTG AAAGAATGGA TTTTCCAGAT CCAGTTATTT      900
CTGTTGCAGT TGAGCCAAAA ACTAAAGCAG ATCAAGAAAA AATGTCTATT      950
GCTTTAAATA AATTAGCACA AGAAGATCCA AGTTTtagag TTTCTACAGA     1000
TGAAGAAAGT GGCCAAACTA TCATTTcagg TATGGGTGAG TTACACCTTG     1050
AAATTATCGT TGATAGAATG CTTCGTGAAT TTAAAGTTGA AGCTGAAGTA     1100
GGTCAACCAC AAGTTGCTTA TCGCGAAACT ATTAGAAAAA CTGTTGAACA     1150
AGAATACAAA TACGCTAAAC AATCAGGTGG TCGTGgTCAG TATGGACATG     1200
TATTCTTACG CCTTGAACCA CTTGAGCCAG GTAGTGATA TGAATTTGTT     1250
AATGATATCA AAGGTGGAGT AATTCCAAAA GAATACATTC CTGCAGTTGA     1300
TAAAGGTGTT CAAGAAGCAT TACAAAATGG TGTTTTAGCA GGTATCCTG     1350
TGGAAGATGT TAAAGTAAC TTTTATGATG GAAGTTATCA CGAGGTGGAT     1400
TCATCTGAGA TGGCGTTTAA ACTTGCTGCT TCTATGGGCT TTAAAGAAGG     1450
TGCTAGAAAA GCAGGTGCTG TGATCTTAGA GCCTATGATG AAAGTTGAAG     1500
TAGAACTCC TGAAGATTAC ATGGGTGATG TTATTGGAGA TCTTAACAAA     1550
CGCCGTGGTC AAGTAAATAG CATGGATGAG CGTGGTGGAA ATAAAATCAT     1600
CACAGCATTT TG                                     1612

```

## 2) INFORMATION FOR SEQ ID NO: 2188

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1667 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni* subsp. *jejuni*  
 (B) STRAIN: ATCC 33560

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2188

ACAATTGAAG	TTGAAAGATC	TATGCGTGTT	CTTGATGGTG	CTGTTGCGGT	50
ATTTTGTTC	GTGGGTGGGG	TGCAGCCTCA	AAGTGAAACA	GTTTGGAGAC	100
AAGCAAATA	ATATGGTGTT	CCAAGAATAG	TATTTGTAAA	TAAAATGGAT	150
AGAATCGGTG	CAAAATTTCTA	CAATGTAGAA	GATCAAATTC	GCAACCGTTT	200
AAAAGCTAAT	CCAGTTCCAC	TTCAAATTC	AATTGGTGCT	GAGGATAATT	250
TTAAAGGCGT	AATCGATCTT	GTAACATGA	AAGCTTTAGT	TTGGGAAGAT	300
GATACTAAGC	CAACGGATTA	TGTAGAAAA	GAAATTCCAG	CTGAACCTAA	350
AGAAAAGGCA	GAAGAATATC	GCACAAAAAT	GATAGAAGCA	GTTTCTGAAA	400
CTTCAGATGA	GTTGATGGAA	AAATATTTAG	GCGGAGAAGA	ATTAAGCCTT	450
GAAGAGATTA	AAACAGGGAT	TAAAGCAGGA	TGTTTAAGTC	TTTCTATCGT	500
TCCTATGCTT	TGCGGTACAG	CGTTTAAAA	TAAAGGGGTT	CAACCTTTGC	550
TTGATGCTGT	TGTGGCTTAT	TTACCAGCTC	CTGATGAAGT	GGCAAATATC	600
AAGGGTGAAT	ATGAAGATGG	CACAGAAGTT	TCTGTAAAAT	CAACTGATGA	650
TGGCGAGTTT	GCAGGACTTG	CATTTAAAA	CATGACAGAT	CCATTTGTAG	700
GACAACTTAC	TTTCGTGCGT	GTTTATCGCG	GTTGTTTAGA	AAGCGTTTCT	750
TATGCGTATA	ACTCAACTAA	AGATAAAAA	GAAAGAATTG	GTCGTTTGTT	800
AAAAATGCAC	TCTAACAAAA	GAGAAGAGAT	TAAAGTGCTT	TACGCAGGCG	850
AAATTGGTGC	TGTTGTAGGA	CTTAAAGATA	CTTTAACAGG	GGATACTCTT	900
GCAAGTGAAA	AAGATAAGGT	AATCCTTGAA	AGAATGGATT	TTCCAGATCC	950
AGTTATTTCT	GTTGCAGTTG	AGCCAAAAAC	TAAAGCTGAT	CAAGAAAAAA	1000
TGTCTATTGC	TTTAAATAAA	TTAGCACAAG	AAGATCCAAG	TTTTAGAGTT	1050
TCTACAGATG	AAGAAAGTGG	TCAAACATATC	ATTTTCAGGTA	TGGGTGAGTT	1100
ACACCTTGAA	ATTATCGTTG	ATAGAATGCT	TTCGTGAATTT	AAAGTTGAAG	1150
CTGAAGTAGG	TCAACCACAA	GTTGCTTATC	GCGAAACTAT	TAGAAAAACT	1200
GTTGAACAAG	AATACAAATA	CGCTAAACAA	TCAGGTGGTC	GTGGTCAGTA	1250
TGGACATGTA	TTCTTACGCC	TTGAACCACT	TGAGCCAGGT	AGTGGATATG	1300
AATTTGTTAA	TGATATCAAA	GGTGGGGTAA	TTCCAAAAGA	ATACATTCCT	1350
GCAGTTGATA	AAGGTGTTCA	AGAAGCATT	CAAAATGGTG	TTTTAGCAGG	1400
TTATCCTGTG	GAAGATGTTA	AAGTAACTGT	TTATGATGGA	AGTTATCACG	1450
AGGTGGATTC	ATCTGAGATG	GCGTTTAAAC	TTGCTGCTTC	TATGGGCTTT	1500
AAAGAAGGTG	CTAGAAAAGC	AGGCGCTGTG	ATCTTAGAGC	CTATGATGAA	1550
AGTTGAAGTA	GAAACTCCTG	AAGATTATAT	GGGTGATGTT	ATTGGAGATC	1600
TTAACAAACG	CCGTGGTCAA	GTAAATAGCA	TGGATGAGCG	TGGTGAAAT	1650
AAAATCATCA	CAGCATT				1667

2) INFORMATION FOR SEQ ID NO: 2189

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1255 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:



- (A) ORGANISM: *Leishmania guyanensis*  
 (B) STRAIN: ATCC 50126

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2189

TGACGGCGCT	GGACGTGACG	GAGGACCTCG	GCCGCGATGA	GCCGCTGACG	50
CTGGAGATCG	TGCAGCACTT	GGATGCGAAC	ACCGGCCGCT	GCATTGCGAT	100
GCAGACGACG	GACCTGCTGA	AGCTGAAGTC	GAAGGTTGTG	TCGACCGGCG	150
GCAACATCTC	CGTGCCGGTG	GGCCGCGAGA	CACTGGGCCG	CATCTTCAAC	200
GTGCTGGGCG	ACGCGATTGA	CCACCGCGGC	CCCGTGTGCG	AGAAGATGCG	250
CATGGCGATC	CACGCCGAGG	CGCCGAAGCT	GGCGGACCAG	GCTGCGGAGG	300
ACACGATCCT	GACGACCGGC	ATCAAGGTGA	TCGACCTGAT	TCTGCCCTAC	350
TGCAAGGGCG	GCAAGATCGG	CCTGTTTCGGC	GGTGCCGGTG	TGGGCAAGAC	400
TGTGATCATC	ATGGAGCTGA	TCAACAACGT	CGCGAAGGGG	CACGGCGGCT	450
TCTCCGTGTT	CGCCGGCGTT	GGCGAGCGCA	CGCGCGAGGG	CACGGACCTG	500
TACCTGGAGA	TGATGCAGTC	AAAGGTGATT	GACCTGAAGG	GCGAGTCGAA	550
GTGCGTGCTT	GTGTACGGGC	AGATGAACGA	GCCCCCGGGT	GCGCGCGCGC	600
GCGTTGCGCA	GTCTGCGCTG	ACGATGGCCG	AGTACTTCCG	CGACGTGGAG	650
GGCCAGAACG	TGCTGCTGTT	CATCGACAAC	ATCTTCCGCT	TCACGCAGGC	700
GAACTCCGAG	GTGTCTGCGC	TGCTGGGCCG	CATCCCGGCC	GCCGTGGGTT	750
ACCAGCCGAC	GCTTGCGGAG	GATCTTGCCA	TGCTGCAGGA	GCGCATTACG	800
TCGACGACGA	AGGGATCGAT	TACGTCTGTG	CAGGCTGTGT	ACGTGCCTGC	850
GGATGATATC	ACGGACCCCG	CGCCGCGGAC	GACGTTCTCG	CACCTGGACG	900
CGACGACTGT	GCTGGACCGC	GCGGTGGCGG	AGTCGGGCAT	CTACCCTGCC	950
GTGAACCCGC	TGGAGTGCGC	GTGCGGCATC	ATGGACCCCG	ATGTGATCGA	1000
CGTGGACCAT	TACAACGTTG	CACAGGATAT	CGTCCAGATG	CTGACCAAGT	1050
ACAAGGAGCT	GCAGGACATC	ATTGCGGTGC	TTGGCATCGA	CGAGCTGAGC	1100
GAGGAGGACA	AGGTCGTGGT	GGACCGCGCG	CGCAAGGTGA	CGCGGTTCCT	1150
GTCGCAGCCG	TTCCAGGTTG	CGGAGGTGTT	CACCGGCATG	ACGGGCCACT	1200
ACGTGCAGCT	GAGCGACACG	GTGGAGTCGT	TCTCTGGCCT	GCTGATGGGG	1250
TCGTA					1255

## 2) INFORMATION FOR SEQ ID NO: 2190

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1248 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma brucei* subsp. *brucei*  
 (B) STRAIN: EATRO 795

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2190

GCCCTTGACG	TTGTTGACAA	ACTTGGCCGT	GATGAGCCTC	TTACTCTTGA	50
GATCGTGACG	CATCTTGACG	CCCACACGGG	CCGCTGTATC	GCGATGCAAA	100
CGACGGATCT	CCTCAAACCTG	AAGGCAAAGG	TCGTTTCGAC	AGGTGGCAAC	150
ATTTCCGTTT	CTGTCGGCCG	GGAAACACTA	GGTCGTATCT	TCAACGTGCT	200
TGGAGACGCT	ATTGACCAGC	GCGGCCCCGT	TGGTGAGAAA	CTGCGCATGC	250
CCATCCATGC	CGTGGCTCCC	AAGCTTGCGG	ACCAGGCCGC	TGAGGATGCG	300
GTGCTCACAA	CTGGTATTAA	GGTGATTGAT	CTCATTCTCC	CTTACTGCAA	350

AGGTGGA	AAA	ATTGGCCTCT	TTGGGGGTGC	GGGTGTGGGC	AAAACCGTCA	400
TTATTATGGA	GCTCATTAAC	AACGTTGCCA	AGGGTCACGG	TGGTTTCTCT		450
GTCTTCGCTG	GTGTTGGTGA	GCGTACCCGT	GAGGGAACGG	ATTTGTATCT		500
TGAGATGATG	CAGTCTAAGG	TTATTGACCT	TAAGGGTGAG	TCCAAATGTG		550
TGTTGGTGTA	CGGTCAGATG	AACGAGCCCC	CAGGTGCCCC	TGCGCGTGTT		600
GCGCAGTCGG	CTCTGACGAT	GGCTGAGTAC	TTCCGTGATG	TGGAGGGCCA		650
AGATGTGCTT	CTTTTATCG	ACAATATTTT	TCGTTTCACT	CAGGCTAACT		700
CCGAGGTGTC	GGCGCTTCTG	GGTCGTATTC	CCGCCGCTGT	TGGCTACCAG		750
CCTACCCTCG	CTGAGGATCT	AGGGCAGTTG	CAGGAGCGTA	TTACCTCAAC		800
AACGAAAGGC	TCCATTACTT	CTGTGCAGGC	CGTATACGTG	CCGGCCGATG		850
ACATTACCGA	TCCAGCTCCA	GCAACAACCT	TCTCACATCT	GGACGCCACA		900
ACTGTGTTGG	ACCGTGCTGT	TGCCGAGTCT	GGTATCTACC	CCGCTGTTAA		950
CCCACTGGAA	TGCGCCTCGC	GTATCATGGA	CCCCGACGTT	ATCAGTGTGG		1000
ATCACTACAA	TGTTGCACAA	GATGTGGTAC	AGATGCTCAC	CAAGTACAGG		1050
GAATTACAGG	ATATCATTGC	TGTCCTTGGT	ATCGACGAGC	TAAGCGAGGA		1100
GGACAAACTT	ATCGTGGACC	GTGCGCGTAA	GTTGGTGAAG	TTCCTCTCCC		1150
AGCCATTCCA	AGTTGCTGAG	GTCTTCACAG	GAATGACTGG	CCATTACGTG		1200
CAGTTGGATG	ACACCATCGA	TTCCTTTTCT	GGTCTCCTCA	TGGGTACG		1248

## 2) INFORMATION FOR SEQ ID NO: 2191

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus nidulans*
- (B) STRAIN: WSA-176

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2191

GAGCTGATTG	TAAGTCATCG	ACCACTTGAT	ATATGAATAC	ATCTAACAGT	50
AGTAGAACAA	CATCGCCAAG	GCTCACGGTG	GTTACTCCGT	CTTCACTGGT	100
GTCGGTGAGC	GTA	CTCGTGA	GGGTAACGAT	CTGTACCACG	150
GACTGGTGTC	ATT	CAGCTCG	ACGGCGAATC	CAAGGTGTCT	200
GTCAGATGAA	CGAGCCCCCA	GGTGCTCGTG	CCCGTGTCGC	CCTTACTGGT	250
CTGACCATCG	CCGAATACTT	CCGTGACGAG	GAGGGTCAGG	ACGTGCTGCT	300
CTTCATTGAC	AACATTTTCC	GTTTCACCCA	GGCCGGTTCC	GAGGTGTCTG	350
CCCTTCTTGG	TCGTATCCCC	TCTGCCGTCG	GTTACCAGCC	CACTCTGGCC	400
GTCGACATGG	GTGGTATGCA	GGAACGTATT	ACCACCACCA		440

## 2) INFORMATION FOR SEQ ID NO: 2192

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1262 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania panamensis*

(B) STRAIN: ATCC 50158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2192

GCTGACGGCG	CTGGACGTGA	CGGAGGACCT	CGGCCGCGAT	GAGCCGCTGA	50
CGCTGGAGAT	CGTGACGAC	TTGGATGCGA	ACACCGGCCG	CTGCATTGCG	100
ATGCAGACGA	CGGACCTGCT	GAAGCTGAAG	TCGAAGGTTG	TGTCGACCGG	150
CGGCAACATC	TCCGTGCCGG	TGGGCCGCGA	GACGCTGGGC	CGCATCTTCA	200
ACGTGCTGGG	CGACGCGATT	GACCACCGCG	GCCCCGTGTG	CGAGAAGATG	250
CGCATGGCGA	TCCACGCCGA	GGCGCCGAAG	CTGGCGGACC	AGGCTGCGGA	300
GGACACGATC	CTGACGACCG	GCATCAAGGT	GATCGACCTG	ATTCTGCCCT	350
ACTGCAAGGG	CGGCAAGATC	GGCCTGTTCT	GCGGTGCCGG	TGTGGGCAAG	400
ACTGTGATCA	TCATGGAGCT	GATCAACAAC	GTCGCGAAGG	GGCACGGCGG	450
CTTCTCCGTG	TTCGCCGGCG	TTGGCGAGCG	CACGCGCGAG	GGCACGGACC	500
TGTACCTGGA	GATGATGCAG	TCAAAGGTGA	TTGACCTGAA	GGGCGAGTCG	550
AAGTGCGTGC	TTGTGTACGG	GCAGATGAAC	GAGCCCCCGG	GTGCGCGCGC	600
GCGCGTTGCG	CAGTCTGCGC	TGACGATGGC	CGAGTACTTC	CGCGACGTGG	650
AGGGCCAGAA	CGTGCTGCTG	TTCATCGACA	ACATCTTCCG	CTTCACGCAG	700
GCGAACTCCG	AGGTGTCTGC	GCTGCTGGGC	CGCATCCCCG	CCGCCGTGGG	750
TTACCAGCCG	ACGCTTGCGG	AGGATCTTGG	CATGCTGCAG	GAGCGCATTA	800
CGTCGACGAC	GAAGGGATCG	ATTACGTCTG	TGCAGGCTGT	GTACGTGCCT	850
GCGGATGATA	TCACGGACCC	CGCGCCCCG	ACGACGTTCT	CGCACCTGGA	900
CGCGACGAT	GTGCTGGACC	GCGCGGTGGC	GGAGTCGGGC	ATCTACCCTG	950
CCGTGAACCC	GCTGGAGTGC	GCGTCGCGCA	TCATGGACCC	CGATGTGATC	1000
GACGTGGACC	ATTACAACGT	TGCACAGGAT	ATCGTCCAGA	TGCTGACCAA	1050
GTACAAGGAG	CTGCAGGACA	TCATTGCGGT	GCTTGGCATC	GACGAGCTGA	1100
GCGAGGAGGA	CAAGGTCGTG	GTGGACCGCG	CGCGCAAGGT	GACGCGGTTT	1150
CTGTGCGAGC	CGTTCCAGGT	TGCGGAGGTG	TTCACCGGCA	TGACGGGCCA	1200
CTACGTGCAG	CTGAGCGACA	CGGTGGAGTC	GTTCTCTGGC	CTGCTGATGG	1250
GGTCGTACGA	CC				1262

2) INFORMATION FOR SEQ ID NO: 2193

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 912 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus nidulans*

(B) STRAIN: WSA-176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2193

TTCCGATGGT	CAAATGTACG	ATTGATATTC	CTTCCAGCCA	GTCAGGATAA	50
CAGCTGATAC	CAGTTGCAAA	TAGGCCCCAG	ACTCGTGAGC	ACTTGTGCT	100
TGCCCCGTCAG	GTTGGTGTCC	AGAAGATCGT	TGTCTTCGTC	AACAAGGTTG	150
ACGCTGTCTGA	TGACCCTGAG	ATGTTGGAGC	TTGTTGAGCT	CGAGATGCGT	200

GAGCTCCTCA	ACACTTACGG	TTTCGAGGGA	GAGGAGACCC	CTATCATCTT	250
CGGTTCCGCC	CTGTGCGCTC	TCGAAGGCCG	CCGCGAGGAC	ATTGGTACTC	300
AGCGTATTGA	CTCCCTCCTC	GAGGCCGTTG	ACACTTGGAT	CCCTACCCCC	350
CAGCGTGACT	TGGACAAGCC	CTTCCTGATG	TCCATTGAGG	AAGTTTTCTC	400
CATTGGTGGT	CGTGGTACCG	TCGCCTCTGG	TCGTGTCGAG	CGTGGTCTCC	450
TCAAGAAGGA	TACCGAAGTT	GAAATTCACG	GTGCTGATGG	TATTCTGAAG	500
ACCAAGGTCA	CCGACATTGA	GACCTTCAAG	AAGAGCTGCG	ATGAGTCTCG	550
TGCTGGTGAC	AACTCCGGTC	TTCTCCTCCG	TGGTATCCGT	CGTGAGGATG	600
TTCGTCGTGG	TATGGTCATC	GCTGCCCTG	GCTCCATCAA	GGCCTCCAAG	650
AAGTTCATGG	TCTCCATGTA	CGTCTTGACT	GAGGCTGAAG	GTGGCCGCAA	700
GAACGGCTTC	GGTGCCAACT	ACCGCCCCCA	GGCTTTCATC	CGCACTGCTG	750
GTAAGTTTCG	AACTATTTGA	TTCATTGATC	ACGTCCCTAA	CTGTTACTTT	800
AGACGAGGCT	TGCGACCTTC	ATTTCCCTGA	TGAGGCCGAC	AAGGACCGCC	850
ACGTCATGCC	CGGTGACAAC	GTCGAAATGG	TCCTCAACCT	CAACAACCCC	900
GTTGCTGCTG	AG				912

## 2) INFORMATION FOR SEQ ID NO: 2194

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 887 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aureobasidium pullulans*
- (B) STRAIN: WSA-234

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2194

TCATCGTCGT	CGCCGCTTCT	GACGGTCAGA	TGCCCCAGAC	CAGAGAGCAC	50
TTGCTTCTCG	CCCGTCAGGT	CGGTATCCAG	AAGATTGTCG	TCTTCGTCAA	100
CAAGGTCGAC	GCCATCGAGG	ACAAGGAGAT	GCTTGAGCTC	GTCGAGATGG	150
AGATGCGTGA	GCTCCTCAGC	AGCTACGGCT	TGAGGGGTGA	CGAGACCCCC	200
ATCGTCATGG	GTTCCGCTCT	TTGTGCCCTT	GAGAACCGCC	AGCCCGAGAT	250
TGGAACCACC	CAGATCGACA	ACCTGATGAA	CGCTGTCGAC	GAGTGGATCC	300
CCACTCCCCA	GAGAGATCTT	GAGAAGCCCT	TCCTCATGTC	CGTTGAGGAT	350
GTCTTCTCTA	TCCCCGGTCG	TGGTACTGTC	GTTTCTGGCC	GTGTTGAGCG	400
TGGTACCCTG	AAGAAGGATT	CCGAAATCGA	GCTTGTCGGC	AAGAACAAGG	450
TCCCCATCAA	GACCAAGGTC	ACCGACATCG	AGACCTTCAA	GAAGTCTTGC	500
GACGAGTCCC	GCGCTGGTGA	CAACTCCGGT	CTTCTGCTCC	GTGGTATCAA	550
GCGTGAGGAT	GTCAACCGTG	GTATGGTTGT	CGTCAAGCCC	GGTACCGTCA	600
CCTCGCACAA	GAAGTTCCTC	GTCTCCATGT	ACGTCCTGAC	CAAGGAGGAG	650
GGTGGTCGTC	ACACTGGTTT	CCACGGAAAC	TACCGTCCCC	AGATCTTCAT	700
CCGTACCGCT	GGTAAGTCCT	GACTTTGAAC	TGCTGACCAA	TTTTCGCATC	750
TCTAACATGT	TTTACAGACG	AGGCTGCCGC	TATTGACTGG	CCCGAAGGCA	800
CCGAGGACGC	TGACTCCAAG	ATGGTCATGC	CCGGTGACAA	CGTCGAGATG	850
GTCTGCTCTC	TTCACAGACC	TCTTGCCGTT	GAACAGG		887

## 2) INFORMATION FOR SEQ ID NO: 2195

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 984 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Emmonsia parva*
- (B) STRAIN: ATCC 10784

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2195

TGACGGCCAA	ATGTAGGACT	CTTGCGCGGG	ACTGACTGAT	TGGGGGGAAT	50
CCATTTTTC	TTTTTCTTT	TTCTTTTGA	GTACATGATT	ATACTAATAT	100
TTGGATAACG	TACCAGGCCT	CAAACACGTG	AACATTTACT	CCTTGCCCGA	150
CAAGTCGGTG	TCCAGAAGAT	CGTCGTTTC	GTAAACAAGG	TCGATGTTCT	200
CGAAGATAAG	GAGATGTTGG	AGCTTGTCGA	GTTGGAAATG	AGAGAGCTCT	250
TGAACACCTA	CGGATTCGAG	GGTGAGGAAA	CGCCCATCAT	CTTCGGTTCT	300
GCCCTTTGTG	CCATGGAGGG	CCGCGAGCCT	GAGCTGGGCG	AGAAGAGAAT	350
TGATGAATTG	CTCGACGCTG	TTGATAGCTG	GATCCCTACG	CCGCAACGTG	400
ATACGGAAAA	ACCCTTCCTA	ATGTCCATTG	AGGAAGTGTT	CTCCATCTCC	450
GGTCGTGGAA	CCGTTGCCTC	CGGCCGTGTT	GAGCGTGGTG	TCCTCAAGAA	500
GGATTCCGAA	GTCGAGCTTG	TTGGCGGCGG	CGTCGCCCCA	ATCAGGACCA	550
AGGTAACCGA	TATCGAAACC	TTCAAGAAGT	CCTGCGACGA	GTCCAGGGCT	600
GGAGACAACT	CTGGCCTTTT	GTTGCGTGGT	GTCAAGCGTG	AGGATATCCG	650
CCGTGGTATG	GTCGTTGTCG	TTCCTGGCAG	CGTCAAGGCC	CACGACAAGT	700
TCTTGGTGTC	CATGTATGTT	CTGACCGAAG	CCGAGGGTGG	TCGCCGAACT	750
GGATTCCGCC	AAAACATATC	TCCTCAAATG	TTTATCCGCA	CAGCTGGTAC	800
GTAACGTATA	ATGCCTCTCC	TCTTCATATA	TACCACCCCC	CCCACCACTG	850
ACTCCCTGAC	TCTTCGATTA	CAGACGAGGC	CGCCGATCTC	AGCTTCCCTG	900
ACGCAGCAGA	CGAAACCAAA	CTGGTTATGC	CCGGTGACAA	CGTCGAGATG	950
ATCCTCAAGA	CACACCGCCC	CATAGCTGCC	GAAG		984

## 2) INFORMATION FOR SEQ ID NO: 2196

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Exserohilum rostratum*
- (B) STRAIN: WSA-215

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2196

GCCGCTCTG	ACGGCCAAAT	GCCCCAGACC	CGTGAGCACT	TGCTGCTTGC	50
TCGCCAGGTC	GGTGTTTACA	AGATTGTTGT	TTTTGTCAAC	AAGGTCGATG	100
CCGTCGAGGA	CAAGGAGATG	TTGGAGCTCG	TTGAGATGGA	GATGCGTGAG	150
TTGCTCAGCA	GCTATGGCTT	CGAGGGCGAT	GAGACTCCCA	TTGTCATGGG	200

CTCCGCTCTC	TGCGCCATCG	AGGGCCGTGA	GCCCGAAATT	GGTGTCAACC	250
GTATTGATGA	GCTGCTCGAG	GCTGTCGACA	CCTGGATCCC	CACCCCTCAG	300
CGTGATACCG	ACAAGCCCTT	CCTCATGGCT	GTTGAGGACG	TCTTCTCCAT	350
TGCTGGCCGT	GGTACCGTCG	TTTCTGGCCG	TGTCGAGCGA	GGTGTCTTGA	400
AGCGCGATGC	CGAAGTCGAG	CTGGTTGGCA	AGGGCACTGC	GCCCATCAAG	450
ACCAAGGTTA	CCGACATTGA	AACCTTCAAG	AAGTCGTGTG	AAGAGTCTCG	500
CGCCGGTGAC	AACTCGGGTC	TCCTCCTCCG	TGGTGTCAAG	CGTGACGACG	550
TCCGCCGTGG	CATGGTCGTT	TCTGTTCTTG	GACAAGTCAA	GGCCCACAAG	600
AAGTTCCTCG	TCTCCATGTA	TGTGTTGAGC	AAAGAGGAAG	GTGGCCGCCA	650
CACGGGCTTC	GGCGAGAACT	ACAGGCCACA	AATGTTTCATC	CGTACTGCTG	700
ACGAGTCATG	CGCGCTGCAC	TGGCCAGAAG	GTACCCCGAG	TGCTCACGAC	750
AAGCTTGTTA	TGCCTGGTGA	TAACGTTGAG	ATGGTTTGTG	AGCTTCACGT	800
GCCACA					806

## 2) INFORMATION FOR SEQ ID NO: 2197

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium moniliforme*
- (B) STRAIN: WSA-213

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2197

ACCCGTGAAC	ACTTGCTCCT	CGCTCGTCAG	GTTGGTGTTC	AGCGAATTGT	50
CGTCTTTGTC	AACAAGGTCG	ATGCCATTGA	TGACCCCGAG	ATGCTTGAGC	100
TCGTGAGAT	GGAGATGCGC	GAGCTTCTTA	ACACCTATGG	CTTCGAAGGC	150
GACGACACTC	CCGTCATCAT	GGGCTCGGCT	CTCATGTCTC	TCCAGAACCA	200
GCGCCCTGAG	ATTGGCACCG	AGAAGATTGA	TGAGCTTCTT	GCTGCCGTCG	250
ACGAGTGGAT	CCCAACCCCC	GAGCGTGACC	TTGACAAGCC	CTTCCTTATG	300
TCCGTCGAGG	ATGTCTTCTC	CATTGCTGGC	CGTGGTACCG	TCGTGTCTGG	350
CCGTGTGGAG	CGTGGTGTTC	TGAAGCGTGA	CCAGGAGATC	GAGCTTGTTG	400
GAAAGGGTCA	GGAGGTTATC	AAGACCAAGG	TTACCGACAT	CGAGACCTTC	450
AAGAAGTCTT	GTGAGCAGTC	CCAGGCTGGT	GACAACTCTG	GTCTCCTCAT	500
CCGAGGTGTT	CGCCGTGAGG	ATGTCCGCCG	TGGTATGGTC	GTCTGCGCTC	550
CTGGCACCGT	GAAGTCTCAC	ACCCAGTTCC	TCGCTTCCCT	CTATGTCCTC	600
TCCAAGGAGG	AGGGTGGCCG	ACACACCGGT	TTCCAGGAGC	ACTACCGACC	650
CCAGCTCTAC	CTCCGAACCG	CAGATGAGTC	CATTGACCTG	ACTTTCCTTG	700
AGGGTACTGA	GGATGCCTCC	AGCAAGATGG	TCATGCCTGG	CGACAACACC	750
GAGATGGTTG	TCACCATGGG	TCACCCCAAT	GCCATCGAGG	TTGGTCAGC	799

## 2) INFORMATION FOR SEQ ID NO: 2198

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium solani*  
(B) STRAIN: ATCC 32793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2198

CTCTGACGGT	CAGATGCCCC	AGACCCGTGA	GCACTTGCTG	CTTGCCCGTC	50
AGGTCGGTGT	CCAGAAGATT	GTCGTCTTCG	TCAACAAGGT	CGATGCCATT	100
GACGACCCTG	AGATGCTTGA	GCTCGTCGAG	ATGGAGATGC	GTGAGCTCCT	150
CAACACCTAC	GGCTTCGAGG	GTGACGAGAC	CCCTGTCATC	ATGGGCTCTG	200
CTCTCATGTC	CCTCCAGAAC	CAGCGCCCCG	AGATCGGTAG	CCAGAAGATT	250
GACGAGCTCC	TTGCCGCCGT	TGACGAGTGG	ATCCCTACCC	CCGAGCGTGA	300
CCTTGACAAG	CCCTTCCTCA	TGTCCGTGTA	GGATGTCTTC	TCCATTGCCG	350
GCCGTGGTAC	CGTCGTCTCT	GGCCGTGTCTG	AGCGTGGTGT	CCTGAAGCGC	400
GACCAGGAGA	TTGAGCTCGT	CGGCAAGGGT	AACGAGGTCA	TCAAGACCAA	450
GGTCACCGAC	ATTGAGACCT	TCAAGAAGTC	TTGCGAGCAG	TCCCAGGCTG	500
GTGACAACTC	TGGTCTCCTC	ATCCGAGGTG	TCCGCCGTGA	GGATGTCCGC	550
CGTGGTATGG	TCGTCTGCGC	CCCCGGCACT	GTCAAGTCCC	ACACTCAGTT	600
CCTTTCTTCC	CTCTACGTCC	TCACCAAGGA	GGAGGGTGGC	CGACACACTG	650
GCTTCCAGGA	GCACTACCGA	CCCCAGCTCT	ACCTCCGAAC	TGCTGATGAG	700
TCCATCGACC	TGACCTTCCC	CGAGGGTACC	GAGGACGCCA	GCAGCAAGAT	750
GGTCATGCCC	GGTGACAACA	CCGAGATGGT	CATCACCATG	GGCCACCCCA	800
ACGCCATTGA	GGTCGGTCA				819

2) INFORMATION FOR SEQ ID NO: 2199

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1025 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Histoplasma capsulatum*  
(B) STRAIN: WSA-377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2199

TGCTGACGGC	CAAATGTAAG	ACGCCGCGAG	GGAGTGCTGA	AGGTTTTATG	50
CTTTTTAGGC	CCTTTGTTTC	TGAGAGCATG	ATGATACTAA	TACTCGGAAA	100
CGTATCTATT	AGGCCTCAAA	CACGTGAGCA	TTTGCTCCTT	GCCCGACAGG	150
TCGGTGTCCA	AAAGATCGTC	GTTTTTCGTGA	ACAAAGTCGA	CGCCCTTGAG	200
GACAAGGAGA	TGTTGGAGCT	TGTCGAGTTA	GAAATGAGAG	AGCTCTTAAA	250
CACCTACGGA	TTTGAGGGTG	AAGAGACACC	CATCATCTTT	GGTCTGCCCC	300
TTTGCGCCAT	GGAAGGCCGT	GAGCCTGAGT	TGGGAGAAAA	GAAAATTGAT	350
GAATTGCTGG	AGGCTGTTGA	TACTTGGATC	CCAACACCAC	AACGTGATAC	400
CGAAAAACCT	TTCTTGATGT	CCGTTGAGGA	AGTATTCTCT	ATCTCCGGTC	450
GTGGAACCGT	TGCCTCCGGT	CGTGTTGAGC	GCGGTGTCCT	CAAGAAGGAT	500

TCAGAAGTCG	AGCTAATTGG	GGGCGGCTCC	ACCCCCATCA	GGACGAAGGT	550
AACTGATATC	GAAACTTTCA	AGAAATCCTG	TGACGAGTCT	AGAGCTGGGG	600
ACAACCTCCG	TCTTTTATTG	CGTGGTATCA	AGCGTGAAGA	TATCCGCCGT	650
GGTATGGTAG	TTGCCGTTCC	TGGCAGCGTC	AAGGCCACG	ACAAGTTCTT	700
GGTGTGATG	TATGTCCTGA	CCGAAGCTGA	GGGTGGTCGC	CGAACCGGAT	750
TCGGCCAGAA	CTATCGTCCT	CAAATGTTCA	TCCGCACAGC	TGGTATGTCA	800
AAATGGGGCC	CCTTTTCATA	ATCCTTTCTT	TTTTTCCTTT	TCCTCTCTCT	850
ATCTCTCTCT	CTGTTTCTTT	TCAACTCGCC	TGATTACAGA	AATTAATAA	900
CCCCTTTGAT	TATAGACGAA	GCCGCCCATC	TCAGCTTCCC	TAGTGGAGCA	950
GATGAAAGCA	AACTCGTTAT	GCCTGGTGAC	AACGTCGAGA	TGATCCTCCA	1000
GACACACCGC	CCCGTGGCTG	CTGAG			1025

## 2) INFORMATION FOR SEQ ID NO: 2200

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kocuria kristinae*
- (B) STRAIN: ATCC 27570

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2200

AGCACGTGCT	GCTCGCCCGC	CAGGTCGGCG	TGCCGACCCT	GCTGGTCGCC	50
CTGAACAAGG	CCGACATGGT	CGAGGACGAG	GAGCTGCTGG	ACCTCGTCGA	100
GATGGAGGTC	CGCGAGCTGC	TGTCCTCCCA	GGAGTTCGAC	GGCGACAACG	150
CCCCCGTCAT	CCGCGTCTCC	GCGCTGAAGG	CGCTGGAGGG	CGACGAGAAG	200
TGGGTCAAGT	CCATCGAGGA	GCTCATGGAG	GCCGTGGACG	AGTACATCCC	250
GGACCCCGTG	CGCGACAAGG	ACAAGCCGTT	CCTGATGCCC	ATCGAGGACG	300
TCTTCACCAT	CACCGGGCGC	GGCACCCTGG	TGACCGGTCG	CGCCGAGCGC	350
GGGACCCTGG	CCCTGAACTC	CGAGGTCGAG	ATCGTCGGCA	TCCGCCCGAT	400
CCAGAAGACC	ACGGTCACCG	GGATCGAGAT	GTTCCACAAG	CAGCTCGACG	450
AGGCCTGGGC	CGGCGAGAAC	TGCGGTCTGC	TGCTGCGCGG	CCTGAAGCGC	500
GACGACGTCG	AGCGCGGCCA	GGTCGTGGTG	AAGCCGGGTT	CCATCACCCC	550
GCACACCAAC	TTCGAGGCGA	ACGTCTACAT	CCTGTCCAAG	GACGAGGGTG	600
GGCGTCACAA	CCCGTTCTAC	TGAACTACC	GTCCGCAGTT	CTACTTCCGG	650
ACCACCGACG	TCACCGG				667

## 2) INFORMATION FOR SEQ ID NO: 2201

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA



## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Vibrio mimicus*  
 (B) STRAIN: ATCC 33653

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2201

TGCTGCAACA	GATGGTCCAA	TGCCACAAAC	TCGTGAGCAC	ATCCTGCTGG	50
GTCGCCAAGT	AGGTATTCCT	TACATCATCG	TATTCATGAA	CAAATGTGAC	100
ATGGTTGACG	ATGAAGAGCT	TCTAGAGCTG	GTTGAGATGG	AAGTTCGTGA	150
GCTTCTGTCT	GAGTACGATT	TCCCAGGTGA	TGACCTGCCA	GTAATCCAAG	200
GTTCAGCACT	AGGCGCGCTA	AACGGCGAAG	CACAGTGGGA	AGCGAAGATT	250
GTTGAACTAG	CAGAAGCACT	AGATTTCATAC	ATTCCAGAGC	CAGAGCGTGC	300
AGTAGACATG	GCATTCCTGA	TGCCAATCGA	AGACGTATTC	TCAATCCAAG	350
GTCGTGGTAC	AGTAGTAACT	GGCCGTATCG	AGCGCGGCAT	CCTGAAAGTG	400
GGTGACGAAG	TTGCGATCGT	TGGTATCAAA	GACACAGTAA	AAACTACCTG	450
TACAGGTGTA	GAAATGTTCC	GTAAGCTGCT	TGACGAAGGT	CGTGCAGGTG	500
AGAACGTTGG	TGCACTGCTA	CGTGGTACTA	AGCGTGAAGA	AGTAGAGCGT	550
GGTCAAGTAC	TGGCGAAGCC	AGGTTCAATC	ACCCACACAC	CTAAGTTCGA	600
ATCAGAAAGTA	TACGTACTGT	CAAAAGACGA	AGGTGGCCGT	CATACTCCAT	650
TCTTCAAAGG	TTACCGTCCA	CAGTTCTACT	TCCGTACAAC	TGACGTAAAC	700
GGCAGCATCG	AGCTTCCAGA	AGGCGTAGAA	ATGGTAATGC	CAGGCGACAA	750
CATCAAGATG	GTTGTAGACC	TGATTGCA			778

## 2) INFORMATION FOR SEQ ID NO: 2202

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter freundii*  
 (B) STRAIN: ATCC 8090

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2202

AACGCTGACC	CTGCAGGTTA	TTGCCGCTGC	GCAGCGTGAA	GGTAAAACCT	50
GTGCATTTAT	CGATGCAGAA	CACGCACTGG	ACCCGGTCTA	TGCCCCGTAAG	100
CTTGGCGTTG	ATATCGATAA	CCTGCTGTGT	TCTCAGCCGG	ATACCGGTGA	150
ACAAGCGCTG	GAAATCTGTG	ATGCACTGGC	GCGCTCCGGT	GCGGTTGACG	200
TTATCGTTGT	CGACTCCGTT	GCCGCATTGA	CGCCGAAGGC	AGAAATCGAA	250
GGCGAGATTG	GCGACTCTCA	CATGGGCCTT	GCGGCGCGTA	TGATGAGCCA	300
GGCGATGCGT	AAGCTGGCCG	GTAACCTGAA	GCAGTCCAAC	ACGCTGCTGA	350
TTTTCATCAA	CCAGATCCGT	ATGAAGATTG	GCGTTATGTT	CGGTAACCCG	400
GAAACCACCA	CC				412

## 2) INFORMATION FOR SEQ ID NO: 2203

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium botulinum*
- (B) STRAIN: 20:1.2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2203

TTTAGATCCA	TCTTATGCTA	GAAATTTAGG	TGTTGATATA	GATAACCTAA	50
TAGTTTCTCA	ACCAGATACA	GGAGAACAGG	CTTTAGAGAT	AACAGAAGCT	100
TTAGTAAGAT	CAGGAGCAGT	AGATGTTATA	GTTGTAGACT	CTGTAGCAGC	150
TTTAGTTTCT	AGGGCAGAAA	TAGAAGGAGA	AATGGGAGAC	TCACATGTAG	200
GTCTTCAAGC	AAGACTTATG	TCTCAAGCCC	TAAGAAAATT	AGCAGGATCT	250
ATAAATAAAT	CTAAGTGTGT	AGCTATATTT	ATAAACCAAT	TAAGAGAAAA	300
GGTTGGTATA	ATGTTTGGAA	ATCCAGAAAC	AACTCCT		337

## 2) INFORMATION FOR SEQ ID NO: 2204

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Francisella tularensis*
- (B) STRAIN: ATCC 29684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2204

AAAGCAAGGC	GGTACTGCAG	CATTTGTTGA	TGCTGAGCAT	GCACTAGATC	50
CAAAATATGC	AAAGCTTTTA	GGTGTTGATG	TTGATAATCT	GATCGTGTCA	100
CAGCCGGATA	CGGGTGAGCA	AGCTTTAGAG	ATTGCTGATA	TGTTGGTACG	150
TTCTGGAGGA	GTTGATATTG	TAGTAATTGA	CTCTGTTGCT	GCACTTACGC	200
CAAAGGCAGA	GATTGAGGGT	GACATGGGCG	ACTCGCACAT	GGGCTTACAA	250
GCAAGATTAA	TGTCACAAGC	ACTAAGAAAA	CTAACGGCAA	ATATCAAGCG	300
CTCAAATACT	CTAGTGATAT	TCATTAACCA	AATTCGTATG	AAGATCGGGG	350
TTATGTTTGG	TAACCCTGAA	ACTACAACT			379

## 2) INFORMATION FOR SEQ ID NO: 2205

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Peptostreptococcus anaerobius*

(B) STRAIN: ATCC 27337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2205

```

ACTTGACCCA GTATATGCAA GGGCTCTTGG AGTGGATATA GACAACCTAG-      50
TCATATCTCA GCCAGATACA GGAGAACAGG CCCTAGATAT AGCAGAGTCC-      100
CTTATAAGAT CAGGAGCTGT AGATATACTA GTAATAGACT CAGTAGCTGC-      150
CCTAGTACCT AAGGCAGAAA TAGAAGGTGA CATGGGAGAT TCTCACGTAG-      200
GTCTACAGGC TAGACTTATG TCACAGGCAC TTAGAAAATT GACTGGATCT-      250
ATAAAGAAGT CAAACTGTGT TGTATATTTT ATCAACCAGT TGAGAGAAAA-      300
AGTAGGGGTT ATGTTTCGGTA ATCCAGAGAC AACAAACA                      337

```

## 2) INFORMATION FOR SEQ ID NO: 2206

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 337 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Peptostreptococcus asaccharolyticus*

(B) STRAIN: LSPQ 2639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2206

```

TCTTGATGCT GGATATGCAA AAAACCTTGG AGTAGATGTA GAAAATTTAA-      50
TTATTTCTCA ACCTGATACA GGTGAGCAAG CCTTAGAAAT AACTGAAGCT-      100
CTTGTAAGAT CTAACGCTGT TGATTTAATT ATTATAGACT CAGTTGCCGC-      150
ACTTGTACCA AAAGCAGAAA TCGATGGTGA CATGGGAGCT GCACAAATAG-      200
GTCTTCAAGC AAGACTTATG TCTCAAGCTC TTAGAAAATT AACTGGGGCA-      250
ATCAACAAGT CAAAATGTAC CGTTGTATTT ATTAACCAAC TTAGAGAAAA-      300
AGTTGGTATC ATGTTTGGTA ACCCAGAAAC TACAACA                      337

```

## 2) INFORMATION FOR SEQ ID NO: 2207

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 408 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Providencia stuartii*

(B) STRAIN: ATCC 33672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2207

CTCACGTTGC	AAGTTATTGC	AGCAGCACAA	CGTAGCGGAA	AAACCTGTGC	50
ATTTATCGAC	GCTGAACATG	CGCTAGATCC	AATCTATGCG	AAAAAACTGG	100
GTGTTGATAT	CGATAACCTT	CTATGTTCTC	AACCTGATAC	TGGTGAGCAA	150
GCATTAGAGA	TTTGTGATGC	ACTGACGCGT	TCAGGCGCTG	TTGATGTCAT	200
TATCGTTGAC	TCCGTGGCCG	CATTAACACC	AAAAGCTGAA	ATTGAAGGTG	250
AAATCGGTGA	CTCACACATG	GGCTTAGCGG	CTCGTATGAT	GAGCCAAGCG	300
ATGCGTAAAT	TAGCGGGTAA	CTTAAAGAAC	TCGAATACAC	TTTTAATCTT	350
CATTAACCAA	ATCCGTATGA	AGATTGGCGT	TATGTTTGGT	AACCCAGAAA	400
CCACTACA					408

2) INFORMATION FOR SEQ ID NO: 2208

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*  
serotype Paratyphi A
- (B) STRAIN: ATCC 9150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2208

GCTGCAGGTG	ATTGCCGCTG	CGCAGCGTGA	AGGTAAAACC	TGTGCGTTTA	50
TCGATGCGGA	ACACGCGCTT	GACCCTGTTT	ACGCACGCAA	GCTGGGCGTC	100
GATATCGATA	ACCTGCTTTG	TTCTCAGCCG	GATACCGGCG	AGCAGGCGCT	150
GGAAATCTGT	GACGCGCTGG	CGCGTTCAGG	CGCGGTGGAC	GTCATTGTGG	200
TCGACTCCGT	AGCGGCGCTA	ACGCCGAAAG	CGGAAATCGA	AGGCGAAATT	250
GGCGACTCTC	ACATGGGCCT	CGCGGCGCGT	ATGATGAGCC	AGGCGATGCG	300
TAAGCTGGCG	GGGAACCTAA	AACAGTCCAA	CACGCTGTTG	ATTTTCATCA	350
ACCAGATCCG	TATGAAGATT	GGCGTGATGT	TCGGTAACCC	GGAAACCACC	400
ACC					403

2) INFORMATION FOR SEQ ID NO: 2209

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*  
 serotype Typhimurium  
 (B) STRAIN: ATCC 14028

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2209

GACCCTGACG	CTGCAGGTGA	TTGCCGCTGC	GCAGCGTGAA	GGTAAAACCT	50
GTGCGTTTAT	CGATGCGGAA	CACGCGCTTG	ACCCTGTTTA	CGCACGCAAG	100
CTGGGCGTCG	ATATCGATAA	CCTGCTCTGC	TCTCAGCCGG	ATACCGGCGA	150
GCAGGCGCTG	GAAATCTGTG	ACGCGCTGGC	GCGTTCAGGC	GCGGTGGACG	200
TCATTGTGGT	CGACTCCGTA	GCGGCGCTAA	CGCCGAAAGC	GGAAATCGAA	250
GGCGAAATCG	GCGACTCTCA	CATGGGCCTC	GCGGCGCGTA	TGATGAGCCA	300
GGCGATGCGT	AAGCTGGCGG	GGAACCTGAA	ACAGTCCAAC	ACGCTGTTGA	350
TTTTCATCAA	CCAGATCCGT	ATGAAGATTG	GCGTGATGTT	CGGTAACCCG	400
GAAACCACCA	CC				412

## 2) INFORMATION FOR SEQ ID NO: 2210

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*  
 (B) STRAIN: ATCC 15305

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2210

ATTAGATCCT	GTTTACGCAG	AAGCTTTAGG	CGTAGATATA	CAAAATTTAT-	50
ATTTATCTCA	ACCTGATCAT	GGGGAACAAG	GTTTAGAAAT	TGCCGAAGCA-	100
TTTGTTAGAA	GTGGCGCTGT	TGATATCGTT	GTGGTCGATT	CAGTTGCTGC-	150
GCTTACACCT	AAAGCTGAAA	TTGAAGGTGA	AATGGGAGAT	ACGCACGTTG-	200
GTTTGCAAGC	ACGTCTTATG	TCCCAAGCCT	TGAGAAAGCT	TTCCGGTGCA-	250
ATTTCAAAAT	CAAATACAAC	AGCAGTATTT	ATCAACCAAA	TCCGTGAAAA-	300
AGTTGGTGTG	ATGTTCCGTA	ATCCTGAAGT	TACACCA		337

## 2) INFORMATION FOR SEQ ID NO: 2211

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia pseudotuberculosis*  
 (B) STRAIN: ATCC 29833

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2211

GACACTGACA	TTACAGGTTA	TCGCCGCCGC	ACAGCGTGAA	GGCAAAACGT	50
GTGCATTTAT	CGATGCCGAA	CATGCCCTTG	ACCCAATCTA	TGCCAAGAAA	100
TTGGGTGTAG	ATATTGATAA	CCTACTGTGT	TCTCAGCCAG	ATACTGGCGA	150
GCAGGCACTG	GAAATTTGTG	ATGCGCTGAC	TCGCTCTGGT	GCGGTTGACG	200
TTATCATCGT	TGACTCCGTA	GCGGCATTGA	CACCAAAAGC	TGAAATTGAA	250
GGTGAAATTG	GCGATTCTCA	TATGGGCCTT	GCCGCGCGTA	TGATGAGCCA	300
GGCTATGCGT	AAGCTGGCGG	GTAACCTGAA	GAATGCGAAT	ACCTTACTGA	350
TTTTTATCAA	CCAAATCCGC	ATGAAAATTG	GCGTGATGTT	TGGTAACCCA	400
GAAACCACTA	CC				412

## 2) INFORMATION FOR SEQ ID NO: 2212

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Zoogloea ramigera*
- (B) STRAIN: ATCC 25935

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2212

CACGCTCACC	TTGCAAACCA	TCGCGGAAAT	GCAAAAACCTG	GGCGGCACCT	50
GCGCGTTTAT	CGACGCCGAG	CACGCACTGG	ACGTCACGTA	CGCGCAAAAG	100
CTGGGCGTCA	ACCTGAGCGA	TCTGCTGATC	TCGCAACCGG	ACACCGGCGA	150
ACAAGCGCTG	GAAATCTGCG	ACGCCCTGGT	GCGTTCCGGT	TCGGTGGACA	200
TGGTCGTGAT	CGACTCGGTC	GCCGCGCTGA	CCCCGCGCGC	CGAGATCGAA	250
GCGGACATGG	GCGATTCGCT	GCCAGGTTTG	CAGGCACGTT	TGATGTCGCA	300
AGCACTGCGC	AAGCTTACCG	GTTTCGATCAA	CCGCACCAAC	ACCCTGGTCA	350
TCTTCATCAA	CCAGATCCGC	ATGAAAATCG	GCGTCATGTT	CGGCAGCCCG	400
GAAA					404

## 2) INFORMATION FOR SEQ ID NO: 2213

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2213

CGTGCCATTG	ACATGATTTC	CGAAGAAGAC	GCTGAAGGCA	CG	42
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## 2) INFORMATION FOR SEQ ID NO: 2214

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia adiacens*
- (B) STRAIN: ATCC 49175

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2214

CAACTACATT ACGTTCTGCA ACACAAGGTC GTGGTACTTT CAGTATGACA	50
TTTGACCACT ATGAAGATGT TCCTAAGAGC ATTGCAGAAG AAATCATCAA	100
GAAAAATGGC GGTAACGGAG AATAA	125

## 2) INFORMATION FOR SEQ ID NO: 2215

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
- (B) STRAIN: ATCC 19606

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2215

C GACTCAAAT GCGTTCTATG TCTCAAGGTC GTGCGACATA CTCAATGGAA	50
TTTGCTAAAT ATGCTGAAAC TCCACGTAAC GTGGCTGAAG GCATCATCGC	100
TAAATTCCAA GCTGGCGGTA AAAAAGGTGA CGACGAGTAA	140

## 2) INFORMATION FOR SEQ ID NO: 2216

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Actinomyces meyeri*  
(B) STRAIN: ATCC 35568

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2216

CCGGTGACCT GCGTTCTAAG ACGCAGGGTC GCGCTGTCTA CTCCATGGAG	50
TTCGACAGCT ACGCCGAGGT TCCGCGCGCG GTCGCGGATG AGATCGTCGG	100
CAAGTCTCGG GGCAACTGA	119

## 2) INFORMATION FOR SEQ ID NO: 2217

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*  
(B) STRAIN: ATCC 9689

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2217

CGACCGACGT TCGCTCCATG TCCCAGGGTC GCGCAAGCTA CTCTATGGAA	50
TTCAAAAAAT ACAACACAGC TCCGGCGCAC ATCGCTGAAA CTGTATCCAA	100
AAAACAAGGC TGA	113

## 2) INFORMATION FOR SEQ ID NO: 2218

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium diphtheriae*  
(B) STRAIN: ATCC 27010

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2218

GCGACCTGCG TTCCCGTACC CAGGGCCGTG CAAACTACAC CATGATCTTC	50
GACTCCTACG CTGAGGTTCC TACCAACGTG GCAGCTGAGA TCGTGGCAGA	100
GCGCAACGGC ACTGCCTAA	119

## 2) INFORMATION FOR SEQ ID NO: 2219

1140



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cloacae*
- (B) STRAIN: ATCC 13047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2219

AACTCAGCTG CGTTCTCTGA CCAAAGGTCG TGCATCATAC ACCATGGAAT	50
TCCTGAAGTA TGATGATGCG CCTAACACG TTGCTCAGGC CGTTATTGAA	100
GCCCGTGGTA AGTAA	115

## 2) INFORMATION FOR SEQ ID NO: 2220

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae pneumoniae*
- (B) STRAIN: ATCC 13883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2220

AACTCAGCTG CGTTCTCTGA CCAAAGGTCG TGCATCATAC ACCATGGAAT	50
TCCTGAAGTA TGATGATGCG CCGAACACG TTGCTCAGGC CGTTATTGAA	100
GCCCGTGGTA AATAA	115

## 2) INFORMATION FOR SEQ ID NO: 2221

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*
- (B) STRAIN: ATCC 15313

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2221

CAACTCACCT	TCG TTCAGGT	ACGCAAGGTC	GTGGTGTATA	CACTATGCAA	50
TTTGACCACT	ATGAAGAAGT	TCCTAAATCT	ATTGCTGAAG	AAATCATTAA	100
AGCTAATGGT	GGA				113

## 2) INFORMATION FOR SEQ ID NO: 2222

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium avium*
- (B) STRAIN: ATCC 25291

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2222

CGGCGACCTG	CGGTCCAAGA	CCCAAGGCCG	GGCGAACTAC	TCCATGGTCT	50
TCGACTCCTA	CGCCGAAGTG	CCGGCCAACG	TGTCGAAGGA	GATCATCGCG	100
AAGGCGACGG	GTCAGTGA				118

## 2) INFORMATION FOR SEQ ID NO: 2223

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium gordonae*
- (B) STRAIN: Mgor-1

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2223

CCGGCGACCT	GCGGTCCAAG	ACGCAAGGCC	GGGCGAACTA	CTCCATGGTG	50
TTCGACTCGT	ACGCCGAAGT	TCCGGCGAAC	GTGTCCAAGG	AGATCATCGC	100
GAAGGCGACG	GGCGAATAG				119

## 2) INFORMATION FOR SEQ ID NO: 2224

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

1142

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium kansasii*

(B) STRAIN: Mkan-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2224

CGGCGACCTG	CGGTCCAAGA	CTCAAGGCCG	GGCGAACTAC	TCGATGGTGT	50
TCGATTCTTA	CGCCGAAGTG	CCGGCTCAGG	TGTCGAAGGA	GATCATCGCG	100
AAGGCGACTG	GCGAGTGA				118

2) INFORMATION FOR SEQ ID NO: 2225

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium terrae*

(B) STRAIN: Mter-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2225

CGGAGACTTG	CGGTCAAGA	CCCAGGGCCG	GGCGAACTAC	TCCATGGTGT	50
TCGACTCCTA	CGCCGAAGTG	CCGGCGCAGG	TGGCGAAGGA	GATTATCGCG	100
AAGGCAACGG	GCGAGTAA				118

2) INFORMATION FOR SEQ ID NO: 2226

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria polysaccharea*

(B) STRAIN: ATCC 43768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2226

GACCGACCTG	CGTTCTGCAA	CCCAAGGCCG	CGCTACTTAC	TCTATGGAGT	50
TCAAGAAATA	TTCTGAAGCT	CCTGCCCCA	TAGCTGCTGC	TGTAAGTAA	100
GCCCGTAAAG	GCTAA				115

## 2) INFORMATION FOR SEQ ID NO: 2227

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*
- (B) STRAIN: ATCC 14990

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2227

AACTTCATTA CGTTCTAACA CGCAAGGTCG CGGTACTTAC ACAATGTACT	50
TTGACCACTA TGCAGAAGTT CCTAAATCAA TTGCTGAAGA AATCATCAAG	100
AAAAATAAAG GTGAATAA	118

## 2) INFORMATION FOR SEQ ID NO: 2228

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
- (B) STRAIN: ATCC 29970

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2228

AACTTCATTA CGTTCTAACA CTCAAGGTCG CGGTACTTAC ACTATGTACT	50
TCGATCACTA TGCAGAAGTT CCAAATCAA TTGCTGATGA TATCATCAAA	100
AAAAATAAAG GTGAATAA	118

## 2) INFORMATION FOR SEQ ID NO: 2229

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1630 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Succinivibrio dextrinosolvens*  
 (B) STRAIN: ATCC 19716

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2229

```

CGTTCAATGC GTGTTCTAGA CGGTGCAGTT ATGGTTTACT GTGCTGTGGG      50
TGGTGTTTCAG CCTCAGTCTG AAACCGTTTG GAGACAGGCT CAGAAGTACA      100
AGGTTCCCTCG TATTGCTTTC GTTAATAAGA TGGACCGTAC TGGTGCTAAT      150
TTCCTACGTG TTGTAGAGCA GATTAAGACC CGTCTAAAGG GTAACCCTGT      200
TCCTCTAATG TTACCTATCG GTAAAGAGGA CAGCTTTGTT GGTGTAGTTG      250
ACCTAATCAA GCGTAAGGCT ATCGACTGGG ATGAGGCATC TCAGGGTATG      300
AAGTTTGAGT ACGTTGACAT TCCAGCAGAT ATGGTTGAGG AAGTTGAAGA      350
GTGGCGTGCA AAGCTTGTA GAGCAGCTGC AGAAGCTAAC GACGAGCTGA      400
TGGATAAATT CTTCGGTGGT GAAGAGCTGA CCGAGGAAGA GATCAAGGCT      450
GCTCTACGTG AGCGTACTCT TCGCAACGAA ATTATTCCTA TGTGCTGCGG      500
TTCAGCATTT AAGAACAAGG GTGTTCAGGC AATGCTTGAC GCTGTTGTTG      550
AGTATCTTCC ATCTCCAGCA GATGTTTCCTG CTGTTGAGGG TAAGACCCTA      600
ACCGGTGAAG CTGATACTCG TAAGGCTGAC GATAAAGAGC CATTCTCTGC      650
TTTAGCATTT AAGCTAGCAA ATGACCCATT CGTAGGTAAC TTAACATTCT      700
TACGTTGCTA CTCAGGCTTT ATTAAGTCTG GTGACACTGT AATGAACTCA      750
GATAAGCAGA AGCGTGAGCG TTTCGGCCGT CTAGTTCAGA TGCACGCTAA      800
TGCTCGTAAT GAGGTTAGCG AGGTTTATGC AGGTGACATC GTTGCTGCTA      850
TTGGTCTGAA GGAAACCGTT ACCGGTGATA CCTTATGTGA CCCAGAGCAT      900
CCAATCATTC TTGAGTCAAT CGACTTTGCA GAGCCAGTTA TCTCTGTAGC      950
AGTTGAGCCT AAGACCAAGG ACGATCAGGA GAAGATGGCT CTTGCTTTAC     1000
AGCGTTTAGC AAAAGAAGAT CCTTCATTCC GCGTTCGTAC AGACGAAGAG     1050
TCTGGCCAGA CCATTATTTT TGGTATGGGT GAGCTTCACC TAGACATCAT     1100
TGTTGACCGT CTACGCCGTG AGTTCAAGGT TGAGTGTAAT CAGGGTAAGC     1150
CACAGGTTGC ATACCGTGAG ACCATTAAGA GCAAGGTTGA ACAGCAAGGT     1200
AAGTTTGCTC GTCAGTCTGG TGGTCGTGGT CAGTACGGTG ACTGCTGGTT     1250
ACGTATGGAA CCTCTTGAGC CAGGTAAGGG CTACGAATTC GTGAATGAGA     1300
TTGTTGGTGG TGTAAATTCCT AAGGAATATA TCCCTGCAAT TGATAAGGGC     1350
TGTCAGGAGC AGATCGCTAA CGGTGTTCTA GCTGGTTTCC CAGTTGTTGA     1400
CATCAAGATC ACTGTATTCG ATGGTTCTTA CCACGAAGTT GACTCTTCAG     1450
AAATGGCATT CAAGATTGCT GCTTCTATGG CATTCAAAGA GGGCTTCAAG     1500
AAGGCAAATC CTGTTCTTCT AGAGCCTTTA ATGAAGGTAG AAGTTGATAC     1550
TCCTGAAGAC TACATGGGTG ACGTTATTGG TGAATTAAAC CGTCGTCGTG     1600
CTATCGTTGA AGGCATGGAA GATGGTCCTA

```

## 2) INFORMATION FOR SEQ ID NO: 2230

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1662 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tetragenococcus halophilus*  
 (B) STRAIN: ATCC 33315

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2230

TTGAAGTGCA	ACGTTTCATTG	CGTGTGCTAG	ACGGTTCAGT	TACTGTCTTG	50
GACTCACAAT	CAGGTGTTGA	ACCACAAACT	GAAACAGTTT	GGCGTCAAGC	100
AACAGAATAT	CAAGTACCTC	GTATTGTATT	CTGTAATAAA	ATGGATAAGG	150
TTGGCGCAGA	TTTCTTATAT	TCTGTCCGAT	CATTGCATGA	TCGTTTAGAA	200
GCTAATGCAC	AACCTATCCA	ATTGCCAATT	GGTGCTGAAG	ATAACTTTGA	250
AGGTATCATC	GACCTTGTGA	AGATGAAAGC	TGAATTTTAT	AAAGATGATT	300
TAGGGACTAC	TTTCGAAGAA	ACTGAAATCC	CAGATGAATA	TAAAGAAACA	350
GCTCAAGAAT	GGCATAATAA	TTTGGTAGAA	TCTGTAGCTG	ATTTTGATGA	400
AGATATCATG	ATGAAATACT	TGGAAGGTGA	AGAAATTACA	CCTGAAGAGT	450
TACAAGCAGG	TATTCGTAAA	GCAACATTAT	CTGTTGAATT	TTACCCAGTA	500
TTATGTGGTT	CTGCATTTAA	AAACAAAGGT	GTTCAAATGA	TGTTGGATGC	550
AGTAATTGAT	TACTTGCTTT	CTCCAACCGA	CGTTCCCCCA	ATTAAAGGGA	600
TCGATCCGAA	AACAGATGAA	GAAACTGAAC	ATCCTGCTGA	TGATAGTGAG	650
CCTTTTTTCAT	CACCTTGCTTT	TAAAGTTATG	TCAGACCCTT	ATGTTGGCCG	700
CTTAACCTTC	TTCCGTGTTT	ATTGAGGTGT	GTTGGATACA	GGTTCCTTATG	750
TATTGAATGC	TACTAAGGGT	TCACGTGAAC	GAATTGGTCG	TATTTTGCAA	800
ATGCATGCCA	ATTCTCGTTC	TGAGATCGAT	AAGGTTTATT	CAGGTGACAT	850
TGCAGCTGCT	GTAGGCTTGA	AGAACACTAC	AACAGGGGAT	ACCCTTTGTG	900
ATGAGAAAAA	TCCAGTTATT	TTGGAAACTA	TCAACTTCCC	TGAACCAGTA	950
ATTCAAGTTG	CTGTTGAACC	TAAGTCAAAA	GCTGACCAAG	ATAAAATGAG	1000
CGTAGCACTA	CAAAAACCTG	CAGAAGAAGA	CCCATCTTTT	AAAGTGGAAA	1050
CCAACGCTGA	AACTGGCGAA	ACTGTAATTG	CTGGTATGGG	TGAACCTCAA	1100
TTAGACGTTT	TTATTGACCG	TATGAAGACT	GAATTTAAAG	TGGATGCCAA	1150
TATTGGTGCA	CCACAAGTTT	CTTATCGTGA	AACTTTCCGT	TCATCAACTA	1200
AAGCTGAAGG	GAAATTTATC	CGCCAATCTG	GTGGTAGAGG	TCAATACGGT	1250
CACGTATGGG	TTGAATTTAC	TCCAACGAA	GAAGGAGCAG	GATTCGAATT	1300
TAAAAACTCC	ATTGTTGGTG	GGGTTGTCCC	TCGTGACTAT	ATACCTGCAG	1350
TACAAAAAGG	ACTGGAAGAC	GCCATGGAAA	ATGGTGTGTT	AGCTGGTTAT	1400
CCATTAGTTG	ACGTAAAGGC	AGAAGTGTTC	GATGGTTCTT	ACCATGACGT	1450
CGACTCTAAT	GAAACAGCCT	TCCGTATTGC	GGCTTCAATG	TCTCTACGTG	1500
AAGCTGCGAA	AAAGGCAGAT	CCAGTTATTC	TTGAACCGAT	GATGAAAGTA	1550
ACAATTAGTA	TCCCTGAAGA	ATATCTAGGT	GATATTATGG	GACATGTTAC	1600
AGCTCGTCGT	GGTCGTGTTG	AAGGAATGGA	TGCTCACGGT	AATGCACAAA	1650
CTGTAAATGC	GT				1662

## 2) INFORMATION FOR SEQ ID NO: 2231

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1652 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Veillonella parvula*
- (B) STRAIN: ATCC 10790

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2231

AAGTAGAACG	TTCTCTACGT	GTAAGTACG	GTTCTGTTGC	GGTGTTTCAGT	50
GCTAAAGGTG	GCGTTGAACC	TCAATCCGAA	ACAGTATGGC	GTCAGGCTTC	100
TAACTACGGC	GTACCTCGTA	TCGCTTATGT	AAATAAGATG	GATACTGTAG	150

GTGCTGACTT	CTTCAACGTA	GTTGACATGA	TGAAAGCTCG	TTTGGGTGCA	200
AATTCCGTAG	CTATCCAAGT	ACCAATCGGT	GCTGAAGATA	CTTTCGAAGG	250
CATCATTGAC	TTGATGACTA	TGAAAGCGGA	AATTTATAAA	TCCGATGACG	300
GTAAAGAATA	TGAAATCACT	GATATCCCTG	CTGAATATCA	AGAAGTAGCA	350
GAAGCTCGTC	GCGAAATGAT	GATCGATGCT	ATCGCTGAAA	CAGATGATGA	400
TATCATGATG	AAATATTTGG	AAGGCGAAGA	AATTTCTGTG	GAAGAATTGA	450
AAGCGGCATT	GCGTAAAGCT	GTTATTGCTA	ACCAATTATT	CCCAGTTCTT	500
TGTGGTTCTT	CCTATAAAAA	TAAAGGTGTT	CAAATGTTAT	TGGATGCTGT	550
TATCGATTAC	ATGCCAGCTC	CAATCGACAT	CCCACCTATT	AAAGGTGTTG	600
TTCCTGGTAC	TGAAGAAGAA	ACAACCTCGTC	CTTCTTCCGA	TGAAGAGCCA	650
TTCTCTGCAT	TGGCATTCAA	AATCATGGCT	GACCCTTATG	TTGGTAAATT	700
AGCGTTCTTC	CGTGTGTACT	CCGGTACATT	GGAATCTGGC	TCCTACGTTT	750
TCAACTCCAC	TAAAGGTAAA	AAAGAACGTA	TCGGTCGTAT	TCTTCAAATG	800
CACGCTAACT	CCCGTAAAGA	AATCGAACGC	GTATATTCTG	GTGACATCGC	850
TGCGGCGGTT	GGCTTAAAGG	ATACTACTAC	AGGCGACACA	TTGTGTGATG	900
AAAAATCTCC	TGTAATCCTT	GAGTCCATGG	AATTCCCTGA	ACCAGTTATC	950
TCCGTTGCTG	TTGAACCTAA	AACAAAAGCT	GACCAAGAAA	AAATGGGTAC	1000
AGCTCTTGCT	CGTTTGGCAG	AAGAAGATCC	TACTTTCAAA	GTTTCGTA CTG	1050
ATGAAGAAGAC	AGGTCAAAC	ATTATCTCTG	GTATGGGCGA	ACTTCACTTG	1100
GATATCATCG	TTGACCGTAT	GAACCGTGAA	TTCAAAGTAG	ATTGTAACGT	1150
AGGTAAACCT	CAAGTAGCAT	ACCGCGAAAC	TATCCGTAAA	GCTGTTAAGG	1200
CTGAAGGTAA	ATTTCGTACG	CAATCTGGTG	GTCGTGGTCA	ATATGGTCAC	1250
TGCTGGTTGG	AATTGATTCC	TCAAGAACCA	GGTGCTGGCT	TCGAGTTTGA	1300
AAACAAGGTT	TAGGTGGTG	CGATTCTCTG	TGAATACATC	GGACCTGTTG	1350
AAAGCGGTGT	TAAAGAAGCT	ATGGAATCCG	GTGTTATCGC	TGGGTACCCT	1400
ATGGTTGATG	TTAAAGTTAT	CGTATTTGAT	GGTTCTTACC	ATGACGTTGA	1450
CTCCAACGAA	ATGGCCTTCA	AAATTGCTGG	TTCTATGGGC	TTCAAAGAAG	1500
GTGCTCGCAA	AGCAGACCCT	GCATTGCTTG	AACCATATAT	GGCTGTAGAA	1550
GTAGACGTTT	CTGAAGAATA	CATGGGCGAC	GTTATCGGTG	ACTTGAAGTC	1600
TCGTCGTGGT	CGCATGGACG	GCATGGAAGC	TCGTAATGGT	TCCCAACATA	1650
TC					1652

## 2) INFORMATION FOR SEQ ID NO: 2232

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1624 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia pseudotuberculosis*
- (B) STRAIN: ATCC 29833

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2232

AGTAGAGCGT	TCCATGCGTG	TTCTTGACGG	CGCGGTAATG	GTTTACTGTG	50
CAGTTGGTGG	TGTTCAGCCA	CAGTCTGAAA	CCGTATGGCG	TCAGGCTAAT	100
AAATATAAAG	TTCCACGTAT	TGCGTTCGTT	AACAAAATGG	ACCGTATGGG	150
TGCGAACTTC	CTGCGCGTAG	TTGGTCAACT	GAAATCTCGC	CTTGGTGCGA	200
ACCCAGTTCC	ACTGCAGTTG	GCAATTGGCG	CAGAAGAAAA	ATTCACCGGT	250
ATTATCGATC	TGGTGAAAAT	GAAAGCGATC	AACTGGAACG	AAGCTGATCA	300
GGGCGTGACC	TTCGAATATG	AAGAAATCCC	TGCTGATATG	GCTGAACTGG	350

CTGCTGAATG	GCACCAGAAT	CTGGTTGAAT	CTGCGGCAGA	AGCGTCTGAC	400
GAGCTGATGG	ACAAATACTT	GGGTGGCGAA	GAGCTGACCG	AAGAAGAAAT	450
CAAGAAAGCT	TTACGTCAAC	GTGTTCTGAA	AAGCGAAATT	ATTCTTGTTA	500
CCTGTGGTTC	TGCGTTTAAA	AACAAAGGCG	TACAGGCAAT	GCTGGATGCG	550
GTTATTGAGT	ACCTGCCTGC	ACCAACTGAC	GTTGAATCAA	TCAACGGCAT	600
CTTGATGAT	GGCAAAGATA	CTCCGGCTGT	TCGTCATTCT	GACGACAAAG	650
AGCCGTTCTC	TGCTCTGGCG	TTCAAAATCG	CTACCGACCC	ATTCGTGGGT	700
AACCTGACGT	TCTTCCGCGT	GTA CTCTGGT	ATTGTTAATT	CCGGTGATAC	750
CGTTCTGAAC	TCAGTGAAAT	CGCAACGTGA	ACGCTTAGGT	CGTATCGTAC	800
AGATGCACGC	TAACAAGCGT	GAAGAGATCA	AAGAAGTTCA	CGCCGGTGAT	850
ATCGCAGCCG	CTATCGGTCT	GAAAGATGTG	ACTACGGGTG	ACACTTTGTG	900
TGACCCGAAT	AATCCGATCA	TCTTGGAACG	TATGGAGTTC	CCAGAGCCGG	950
TAATCTCTGT	TGCTGTTGAA	CCAAAAACCA	AAGCTGACCA	AGAAAAAATG	1000
GGTATGGCTC	TGGGGCGTTT	GGCGAAAGAA	GATCCATCAT	TCCGCGTTTG	1050
GACTGACGAA	GAATCTGGTC	AGACTATCAT	CGCTGGTATG	GGTGAGTTGC	1100
ATTTGGATAT	CCTGGTTGAC	CGTATGCGCC	GCGAATTTAA	CGTGGAAGCA	1150
AACGTCGGTA	AACCTCAGGT	TGCGTACCGT	GAAACTATCC	GCGAAACCGT	1200
TAAGGATGTG	GAAGGTAAGC	ACGCTAAGCA	GTCAGGCGGT	CGTGGTCAGT	1250
ATGGTCATGT	TGTTATCGAC	ATGTCTCCAT	TGCCACCGGG	TGGTGTTGGG	1300
TATGAATTCG	TCAACGAAAT	CGTTGGTGGT	TCTATTCCTA	AAGAATTCAT	1350
TCCGGCCGTT	GATAAAGGTA	TTCAAGAACA	GCTGAAATCT	GGCCCTCTGG	1400
CAGGTTACCC	AGTTGTTGAC	GTTAAAGTGC	GTCTGCACTA	CGGTTCTTAC	1450
CATGACGTTG	ACTCCTCAGA	ATTGGCATT	AAATTAGCTG	GTTCTATCGC	1500
CTTTAAAGAA	GGTTTCAAAC	GAGCTAAACC	AGTTCTGCTT	GAGCCAATCA	1550
TGAAGGTTGA	AGTCGAAACC	CCTGAAGATT	ACATGGGTGA	CGTAATGGGC	1600
GACCTGAACC	GTCGTCGCGG	TATC			1624

## 2) INFORMATION FOR SEQ ID NO: 2233

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1636 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Zoogloea ramigera*
- (B) STRAIN: ATCC 25935

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2233

GAACGCTCGA	TGCGCGTGCT	TGACGGTGCT	TGCATGGTTT	ACTGCGCAGT	50
GGGCGGTGTT	CAGCCACAGT	CGGAAACCGT	GTGGCGTCAG	GCTAACAAGT	100
ACAAAGTGCC	ACGTCTGGCC	TTCGTCAACA	AGATGGACCG	TACCGGCGCC	150
AACTTCTTCA	AGGTGTACGA	GCAGATGCGT	GCTCGCCTGA	AGGCCAACCC	200
GGTCCTGATC	CAGATCCCTA	TCGGCGCTGA	AGACAACTTC	AAAGGCGTGA	250
TCGATCTGGT	CAAGATGAAG	GCTATCCTGT	GGGACGAAGC	GTGCAAGGC	300
ATGAAATTCG	ACTACGTCGA	TATTCCTGCA	GAGCTGGCTG	ATTCGGCCGC	350
CGAGTGCGCG	GAAAAGATGG	TTGAAGCTGC	TGCTGAAGCC	ACCGAAGAGC	400
TGATGAACAA	GTACCTGGAA	GAAGGCGACC	TGACCGAAGC	CGAGATCAAG	450
CAGGCGCTGC	GTACCCGTAC	CATCGCTTCG	GAAATCGTTC	CGATGATGTG	500
CGGTACCGCC	TTCAAGAACA	AGGGCGTACA	GGCCATGCTG	GACGCGGTCA	550
TCAATACCT	GCCATCGCCA	CTGGACATCG	ACGATGTCGG	CGGTACGGAC	600



GAAGACGACC	AGCCAACCAC	CCGTCGCGCA	GCTGACGACG	AGAAATTCTC	650
GGCGCTGGCC	TTCAAGATCA	TGACCGACCC	GTTCGTCGGT	CAATTGGCCT	700
TCTTCCGCGT	GTACTCGGGC	GCCGTCAATT	CGGGCGACAC	CGTGTACAAC	750
TCGGTCAAAG	GTCGTAAAGA	GCGTCTGGGC	CGTATTCTGC	AGATGCACGC	800
GAATCAGCGC	GAAGAGATCA	AAGAAGTGCG	CGCCGGCGAC	ATCGCCGCTG	850
CGGTTGGCCT	GAAAGACGTG	ACCACGGGCG	AAACCCTGTG	CGATCCGACC	900
GCCATCATCA	CGCTGGAAAA	AATGATCTTC	CCTGAGCCTG	TGATTCAACA	950
GGCAGTCGAG	CCAAAAACCA	AGGCCGACCA	GGAAAAAATG	GGCCTGGCAC	1000
TGAACCGCCT	GGCACAGGAA	GATCCTTCGT	TCCGCGTGAA	GACCGATGAA	1050
GAATCGGGCC	AGACCATCAT	CGGTGGWATG	GGCGAGCTGC	ACCTGGAAAT	1100
TATCGTTGAC	CGCATGAAGC	GCGAATTCGG	CGTGGAAGCA	ACCGTCGGCA	1150
AGCCACAAGT	GGCTTACCGC	GAAACGATCC	GTAAAACCTG	CGAAGAATCG	1200
GAAGGCAAGT	TCGTCAAGCA	ATCCGGTGGT	CGTGGTCAAT	ACGGTCACGT	1250
TGTGCTGAAG	ATCGAGCCGC	AAGAACCAGG	CAAGGGCTTC	GAGTTCGTTG	1300
ACGCCATCAA	GGGCGGTACC	GTTCTTCGCG	AGTACATCCC	TGCGGTGGAA	1350
AAAGGCGTGC	GCGGCACCCT	GAACACCGGC	GTGCTGGCTG	GTTACCCGGT	1400
CGTGGACGTC	AAGGTCACGC	TGTTCTTCGG	TTCGTACCAC	GATGTGGACT	1450
CGAACGAAAA	CGCGTTCCAG	ATGGCCGCTT	CGATGGCATT	CAAAGAAGGC	1500
TGCCGCAAAG	CATCGCCAGT	CATTCTGGAG	CCAATGATGG	CTGTGGAAGT	1550
GGAACGCCCG	GAAGACTACG	CCGGTACCGT	GATGGGCGAC	CTGTCGTCCC	1600
GCCGCGGTAT	GGTGCAGGGC	ATGGACGAAA	TCCCAG		1636

## 2) INFORMATION FOR SEQ ID NO: 2234

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1656 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aeromonas hydrophila*
- (B) STRAIN: ATCC 7966

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2234

GGCACGAACG	ATCTTGCCGG	ACGGGCCATC	TTCCATACCT	TCGATCAGGC	50
CACGACGACG	GTTCAGGTCA	CCGATCACGT	CGCCCATATA	GTCTTCCGGA	100
GTCTCGACTT	CTACTTTCAT	GATCGGTTTCG	AGCAGAACCG	GGTTGGCCTT	150
CATGAAGCCA	GCCTTAAAGG	CCATGGAAGC	AGCGATCTTG	AACGCCAGTT	200
CGGAAGAGTC	GACATCGTGG	TAGGAACCGA	AGTGCAGACG	CACGCCCAGA	250
TCCATAACCG	GATAACCTGC	CAGCGGGCCG	GACTTCAGTT	GCTCGCGGAT	300
ACCCTTGTC	ACACCCGGGA	TGAACTCACC	AGGAATGACG	CCGCCCTTGA	350
TGTCGTTGAC	GAATTCGTAG	GCTTTGCCTT	CTTCCAGCGG	GTACATGTTCG	400
ATCACAACGT	GACCGTACTG	ACCACGACCA	CCGGACTGCT	TGGCGTGCTT	450
ACCTTCGATA	TCCTTGACGG	TGTTACGAAT	GGTTTCACGG	TAGGCAACCT	500
GCGGCTTACC	TACGTTTCGCT	TCTACCTTGA	ACTCGCGACG	CATACGGTCA	550
ACGATGATGT	CCAGGTGCAG	CTCACCCATA	CCGGCGATGA	TGGTTTGGCC	600
AGACTCTTCG	TCAGTCCATA	CGCGGAAGGA	CGGGTCTTCC	TGAGCCAGAC	650
GGCCCAGAGC	CAGGCCCATC	TTCTCTTGGT	CAGCCTTGGT	TTTCGGCTCA	700
ACTGCGATGG	AGATTACCGG	TTCCGGGAAT	TCCATACGCT	CGAGGATGAT	750
CGGCGCTTTT	TCGTCACACA	GGGTGTCACC	GGTGGTCACG	TCTTTCAGAC	800
CAATGGCGGC	AGCGATGTTCG	CCTGCGCGAA	CTTCTTTGAT	CTCTTCACGC	850

TTGTTGGCGT	GCATCTGAAC	GATACGGCCA	AAACGCTCGC	GCTTCTCTTT	900
AACGGAGTTC	AGCACGGAGT	CACCGGAGTT	AACCACACCG	GAGTAAACGC	950
GGAAGAAGGT	CAGGTTGCCT	ACGAACGGGT	CGGTAGCAAT	CTTGAATGCC	1000
AGAGCAGCAA	ACGGCTCGTC	ATCAGAAGCA	TGACGCTCGT	CTTTGGTCTC	1050
GCCATCCAGC	TTCAGACCGT	CGATGGCTGC	TACGTCGGTC	GGCGCCGGCA	1100
GATAGTCAAC	CACGGCATCC	AGCATGGCCT	GTACGCCCTT	GTTCTTGAAC	1150
GCGGAGCCAC	AGGTAACCAG	GATGATTTTC	TTGTTTCAGAA	CACGCTGACG	1200
AAGAGCTTTC	TTGATCTCTT	CCTCGGTCAG	TTCTTCACCA	CCCAGGTATT	1250
TTTCCATCAG	GTCTTCAGAC	GCTTCAGCAG	CGGCTTCAAC	CAGGGTCATG	1300
CGCATTTCTT	GCGCTTTTTC	CAGCAGCTCA	GCCGGGACGT	CTTCGTAATC	1350
GAAGGATACG	CCCTGGTCAG	CTTCGCTCCA	GTTGATGGCT	TTTCATCTTGA	1400
CCAGGTCGAT	AACGCCCTTG	AAGTTCTCTT	CTGAACCGAT	GTTTCAGTTGC	1450
AGCGGAACCG	GGTTACCTTT	CAGACGGGTC	TTGATGTGCT	CAACGCAGCG	1500
CAGGAAGTTG	GCACCGGTAC	GGTCCATCTT	GTTGACGAAC	GCGATACGGG	1550
GAACCTTGTA	CTTGTTAGCC	TGACGCCATA	CGGTTTCAGA	CTGTGGCTGT	1600
ACGCCACHTA	CGGCACAGTA	CACCATCACG	GCGCCGTCCA	GAACACGCAT	1650
GGAACG					1656

## 2) INFORMATION FOR SEQ ID NO: 2235

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia adiacens*
- (B) STRAIN: ATCC 49175

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2235

TCTCCTCCCC	ATTTGATAAC	TACCAAATGA	ACGCTATCGA	CTGGTTATGT	50
CAGTCATAAC	CAGTTGATTT	TTAAGAGAGT	TCTTTGGTAT	AATTACAATC	100
GGTAGATACT	GTTATAGAAT	CTAACAAAAC	TCAATTAATA	GGAGGAATCA	150
TTTAA					155

## 2) INFORMATION FOR SEQ ID NO: 2236

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
- (B) STRAIN: ATCC 19606

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2236

TCTTTCGATT ACTATAAGCC CTAATAATT CTTAGTTAAA AACCAAGTGC	50
TCATGGAGCG ACCCTCCATG AGTAGTTAAT AAAGGAAGAT CATC	94

## 2) INFORMATION FOR SEQ ID NO: 2237

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Actinomyces meyeri*
- (B) STRAIN: ATCC 35568

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2237

GTCCCACCGG GGGTGAGTGG GGGCCGGGCA ATCGGCCCCCT GCGAGCCGCC	50
TCACACACCA GTAATCCCAG TAGGTCTCAT GCCCATGGG TGTAAAGTG	100
ACACCTAGCC GTAGGCTGAG AATTCTACC CGAGTCCAGG AGGACGAAAA	150

## 2) INFORMATION FOR SEQ ID NO: 2238

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: ATCC 9689

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2238

TTCAGTCCTT TAGGCAAGGA GTTAATTGTC	30
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## 2) INFORMATION FOR SEQ ID NO: 2239

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium diphtheriae*  
 (B) STRAIN: ATCC 27010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2239

CAACTAGCCT	CTCGCTTATC	TCCCTATGCA	AAATTTCTAG	TCAGTTACAG	50
GGCATAGGGG	GAGCGTAGGC	GGGGGTAGCG	GCTTGCTGAG	CACTTCCTCT	100
ACATCAAAGG	GAATGTTGAG	CCGGCCGTTA	CCCTGTACGA	TCCCATCTGG	150
TTTCTTCGGT	GGTTTGATAA	ATACCCCGTT	GTGACCCTAG	GATCATGTAA	200
CTGGCACAAT	GTAAATAGCT	GTACTGCCAG	GCTGCCGAAT	TAGCAGTCAG	250
AAATGTACAG	CACTGTCAAC	TCGTGGCTGC	GAAATCGTAG	CCACCACGAA	300
GTCCAGGAGG	ACACACA				317

## 2) INFORMATION FOR SEQ ID NO: 2240

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cloacae*  
 (B) STRAIN: ATCC 13047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2240

TCCACAGGAT	TAAAACCTAA	GTCCCGTGCT	CTCTCCTGAG	GGGAGAGCAC	50
TATAGTAAGG	AATATAGCC				69

## 2) INFORMATION FOR SEQ ID NO: 2241

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*  
 (B) STRAIN: ATCC 13883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2241

TCCACAGGAT	TAAAACCTAA	GTCCCGTGCT	CTCTCCGAAG	GGGAGAGCAC	50
TATAGTAAGG	AATATAGCC				69

## 2) INFORMATION FOR SEQ ID NO: 2242

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*
- (B) STRAIN: ATCC 15313

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2242

AACAACAAAG AAGATTAATT GATTTTTTTC GCAACATCAA GTATAACTTT	50
AGTTAGAAGT ATTACTTAGT TTAAATTTAA GCTAAGTAAA AAATAATTAT	100
CGAATTATCG AGGAGGATAT TTAAAA	126

## 2) INFORMATION FOR SEQ ID NO: 2243

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium avium*
- (B) STRAIN: ATCC 25291

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2243

GTGTCAACTC ACTGGCTCGG AGCCGAGCAA TCGGCTCAGC GAAGGCGACG	50
GGTCAGTAGC TACTGGCAGC GGAGTAATCT TGCCGGGTCA TTGGAATGCC	100
TTGGGCGCGG CACAACTGAA AACACCAACA CTGCTTTAAC AAGCACCAAC	150
TAGTCCAGGA GGACACAGAA	170

## 2) INFORMATION FOR SEQ ID NO: 2244

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

1153

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium gordonae*  
(B) STRAIN: Mgor-1

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2244

```
GGCCGGCAAG CCTGCGAGTA AGCTGACGCG GTTAGCACCG CGGCAAAACC      50
AAGAAAAATC AACACTGCTT TTTTAAGCAC CAACAGTCCA GGAGGACAAC      100
AAA                                                    103
```

## 2) INFORMATION FOR SEQ ID NO: 2245

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium kansasii*  
(B) STRAIN: Mkan-1

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2245

```
GCCGAGCGTT GCGCGTAAGC TAGCTCGGTT ACCACGGCGG CAAAAC TAGA      50
AAACATCAA CACTGCTTTT ATAAGCACCA ACAGTCCAGG AGGACACAGA      100
A                                                    101
```

## 2) INFORMATION FOR SEQ ID NO: 2246

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium terrae*  
(B) STRAIN: Mter-1

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2246

```
CCAGCTTCCC GCCCGTGCCG CTACGGTGGC ACAAACCCAA AAAGATCAAT      50
CCTGCTGTAA CCCAGCACCA ACAAGTCCAG GAGGACAAGA A                91
```

## 2) INFORMATION FOR SEQ ID NO: 2247

1154

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria polysaccharea*
- (B) STRAIN: ATCC 43768

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2247

TCAGGCAAAT AGGCCGTCTG AAAGGCTGAA ATGATTTTTC AGACGGCATT	50
GTTCTTTAAT CGATCTTTAA TGTAAGGAA TTAGCTC	87

## 2) INFORMATION FOR SEQ ID NO: 2248

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*
- (B) STRAIN: ATCC 14990

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2248

TATAACTTGT TAAGACTAGC TATGCTAGGT TAAAATACAG GTTGAGCTTA	50
TTTATAAGCT GACATTTTTA TGATTTGATT TTTAGGGGTA AATGCATTAT	100
AAAAGAATTA TAAATTCTTT TATGCTACAC TCAATCAATT TTCTTCTCAT	150
GATGGTGAGA AACTATCATG AGAGATAAAT TTGAAATAAC TTTTATTAAG	200
AATAGGAGAG ATTTAATA	218

## 2) INFORMATION FOR SEQ ID NO: 2249

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
- (B) STRAIN: ATCC 29970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2249

TTAAACTTGT	TTTAGCTAGA	ATTTCTAGGT	AAAATACAGC	GTAAGCTTAT	50
TAATTAAGCT	AACATCTTTA	TGAATTGATT	TTTTACTGAA	AATGCATTAT	100
AAATGAATTA	TGAATTCTAA	CAATCATTAT	GTCTCATGAT	GGTGAGAAAC	150
TATCATGAGA	GATAATATTG	AAATAACTTT	TACTAGAATA	GGAGAGATTT	200
AATA					204

2) INFORMATION FOR SEQ ID NO: 2250

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2250

CCGTCGGATG GTGTCGTATA CCGCGGAGTC GCCGACGG 38

2) INFORMATION FOR SEQ ID NO: 2251

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2251

CGGAGCCGTT CTCGCTGCGT TACATGCTGG TGGCTCCG 38

2) INFORMATION FOR SEQ ID NO: 2252

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2252

CCACATACAG TGTCTCTC 18



## 2) INFORMATION FOR SEQ ID NO: 2253

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2253

CATTACCCAA CCGAAAGTA

19

## 2) INFORMATION FOR SEQ ID NO: 2254

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2254

ACCTGAACAG AGAGAAATG

19

## 2) INFORMATION FOR SEQ ID NO: 2255

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia adiacens*
- (B) STRAIN: ATCC 49175

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2255

ATGGCAAAAG	AAAAATTTGA	CCGTTCAAAA	CCACACGTTA	ACATTGGTAC	50
AATCGGCCAC	GTTGACCACG	GTAAAACAAC	ATTAAGTGCT	GCTATCACAA	100
CTGTTTTAGC	TAAGAAAGGT	TTCGCGCAAG	CTCAAGATTA	CGGTTCAATC	150
GATAAAGCTC	CAGAAGAACG	CGAACGTGGT	ATCACAATCA	ACACTTCTCA	200
CGTTGAGTAC	GAAACAGACA	CTCGTCACTA	TGCTCACGTT	GACTGCCCAG	250
GACACGCGGA	CTACGTTAAA	AAC			273

## 2) INFORMATION FOR SEQ ID NO: 2256

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
- (B) STRAIN: ATCC 19606

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2256

ATGGCTAAAG	CCAAGTTTGA	ACGTAATAAA	CCACACGTAA	ACGTGGGTAC	50
AATCGGTCAC	GTTGACCATG	GTAAAACAAC	TTTAACTGCT	GCGATTGCAA	100
CAATTTGTGC	AAAAACTTAC	GGCGGTGAAG	CGAAAGATTA	CTCACAAATC	150
GACTCAGCAC	CTGAAGAAAA	AGCACGTGGT	ATTACAATTA	ATACATCACA	200
CGTAGAATAC	GATTCTCCAA	CTCGTCACTA	CGCACACGTT	GACTGCCCAG	250
GCCACGCCGA	CTACGTTAAA	AAC			273

## 2) INFORMATION FOR SEQ ID NO: 2257

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Actinomyces meyeri*
- (B) STRAIN: ATCC 35568

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2257

GTGGCGAAGG	CCAAGTTTGA	GCGCACCAAG	CCGCACGTCA	ACATCGGCAC	50
GATTGGTCAC	GTTGACCACG	GCAAGACGAC	GCTGACGGCA	GCTATCACCA	100
AGGTGCTGCA	TGACAAGTAC	CCCGAACTGA	ACGAGTTCAC	CCCCTTCGAT	150
CAGGTCGACA	ACGCTCCCGA	GGAGCGCGAT	CGTGGCATCA	CGATCAACGT	200
CTCTCACGTT	GAGTACCAGA	CCGAGGCGCG	TCACTACGCG	CACGTTGACG	250
CTCCCGGCCA	CGCCGACTAC	GTCAAGAAC			279

## 2) INFORMATION FOR SEQ ID NO: 2258

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: ATCC 9689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2258

GTGGCTAAAG	AAAAATTTGA	TCGTTCCCTA	CCGCACGTCA	ACGTTGGCAC	50
TATCGGTCAC	GTTGACCATG	GTAAAACCAC	TCTGACTGCT	GCTCTGACTC	100
GCGTTTGCTC	CGAAGTATTC	GGTTCCGCAA	TCGTTGATTT	CGATAAAATC	150
GACAGCGCAC	CAGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACCGCGCA	200
CGTTGAATAC	AACTCGCTGA	TCCGTCAC	CGCTCACGTT	GACTGCCCAG	250
GTCACGCTGA	CTATGTGAAG	AAC			273

## 2) INFORMATION FOR SEQ ID NO: 2259

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium diphtheriae*
- (B) STRAIN: ATCC 27010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2259

GTGGCAAAGG	CTAAGTTCGA	GCGTACCAAG	CCGCACGTCA	ACATCGGCAC	50
CATCGGTCAC	GTTGACCACG	GTAAGACCAC	CACCACCGCT	GCTATCACCA	100
AGGTTTTTGGC	AGACGCTTAC	CCAGAGCTGA	ACGAAGCTTT	CGCTTTCGAT	150
GCCATCGATA	AGGCACCGGA	AGAGAAAGAG	CGTGGTATTA	CCATCAACAT	200
CTCCACCGTG	GAGTACCAGA	CCGAGAAGCG	CCACTACGCA	CACGTTGACG	250
CTCCAGGTCA	CGCTGACTAC	ATCAAGAAC			279

## 2) INFORMATION FOR SEQ ID NO: 2260

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cloacae*  
 (B) STRAIN: ATCC 13047

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2260

GTGTCTAAAG	AAAAATTTGA	ACGTACAAAA	CCGCACGTCA	ACGTTGGTAC	50
TATCGGCCAC	GTTGACCATG	GTAAAACTAC	CCTGACTGCT	GCAATCACTA	100
CCGTTCTGGC	TAAAACCTAC	GGTGGTTCTG	CTCGTGCATT	CGACCAGATC	150
GATAACGCAC	CAGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACCTCTCA	200
CGTTGAATAT	GACACCCCGA	CTCGCCACTA	CGCACACGTA	GACTGCCCAG	250
GTCACGCCGA	CTATGTTAAA	AAC			273

## 2) INFORMATION FOR SEQ ID NO: 2261

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*  
 (B) STRAIN: ATCC 13883

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2261

GTGTCTAAAG	AAAAATTTGA	ACGTACAAAA	CCGCACGTCA	ACGTTGGTAC	50
TATCGGCCAC	GTTGACCATG	GTAAAACTAC	CCTGACTGCT	GCCATCACTA	100
CCGTTCTGGC	TAAAACCTAC	GGTGGTTCCG	CTCGCGCATT	CGACCAGATC	150
GATAACGCAC	CGGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACCTCTCA	200
CGTTGAATAT	GACACCCCGA	CTCGCCACTA	CGCGCACGTA	GACTGCCCCG	250
GCCACGCCGA	CTATGTTAAA	AAC			273

## 2) INFORMATION FOR SEQ ID NO: 2262

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*  
 (B) STRAIN: ATCC 15313

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2262

ATGGCAAAAG	AAAAATTTGA	CCGCTCTAAA	CCCCATGTTA	ACATTGGTAC	50
TATTGGACAC	GTTGACCATG	GTAAACAAC	TTTAACTGCT	GCAATTACAA	100

CTGTACTTGC	TAAAAAAGGC	TATGCTGATG	CACAAGCTTA	TGACCAAATT	150
GATGGTGCTC	CAGAAGAAAG	AGAACGTGGA	ATCACAATCT	CTACTGCTCA	200
CGTTGAGTAC	CAAAC TGACA	GCCGTCAC TA	TGCACACGTT	GACTGCCCAG	250
GACATGCCGA	TTACGTTAAA	AAC			273

## 2) INFORMATION FOR SEQ ID NO: 2263

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium avium*
- (B) STRAIN: ATCC 25291

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2263

GTGGCGAAGG	CGAAGTTCGA	GCGGACGAAG	CCGCACGTCA	ACATCGGGAC	50
CATCGGTCAC	GTTGACCACG	GCAAGACCAC	GCTGACCGCG	GCTATCACCA	100
AGGTTCTGCA	CGACAAGTAC	CCGGACCTGA	ACGAGTCCCG	CGCGTTCGAC	150
CAGATCGACA	ACGCGCCCGA	GGAGCGTCAG	CGCGGTATCA	CCATCAACAT	200
CTCCCACGTG	GAGTACCAGA	CCGACAAGCG	GCACTACGCT	CACGTCGACG	250
CCCCGGGTCA	CGCCGACTAC	ATCAAGAAC			279

## 2) INFORMATION FOR SEQ ID NO: 2264

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium gordonae*
- (B) STRAIN: Mgor-1

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2264

GTGGCGAAGG	CGAAGTTCCA	GCGGACCAAG	CCGCACGTCA	ACATCGGGAC	50
CATCGGTCAC	GTTGACCACG	GCAAGACCAC	TCTGACCGCG	GCTATCACCA	100
AGGTCCTGCA	CGACAAGTAC	CCGGACCTGA	ACGAGTCCAA	GGCGTTCGAC	150
CAGATCGACA	ACGCGCCTGA	GGAGCGTCAG	CGCGGTATCA	CGATCAACAT	200
CGCGCACGTG	GAATACCAGA	CCGAGAAGCG	TCACTACGCG	CACGTCGACG	250
CCCCCGGCCA	CGCCGACTAC	ATCAAGAAC			279

## 2) INFORMATION FOR SEQ ID NO: 2265

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium kansasii*
- (B) STRAIN: Mkan-1

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2265

GTGGCGAAGG	CGAAGTTCCA	GCGGACCAAG	CCCCACGTCA	ACATCGGGAC	50
CATCGGTAC	GTTGACCACG	GCAAGACCAC	CCTGACCGCG	GCTATCACCA	100
AGGTCCTGCA	TGACAAGTTC	CCGGACCTGA	ACGAGTCGAA	GGCGTTCGAC	150
CAGATCGACA	ACGCTCCTGA	GGAGCGCCAG	CGCGGTATCA	CGATCAACAT	200
CGCGCACGTG	GAGTACCAGA	CCGAGAAGCG	GCACTATGCA	CACGTCGACG	250
CGCCGGGCCA	CGCCGACTAC	ATCAAGAAC			279

## 2) INFORMATION FOR SEQ ID NO: 2266

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium terrae*
- (B) STRAIN: Mter-1

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2266

GTGGCGAAGG	CGAAGTTCTGA	GCGGACGAAG	CCGCACGTCA	ACATCGGGAC	50
CATCGGTAC	GTTGACCACG	GCAAGACCAC	GCTGACCGCG	GCTATCACCA	100
AGGTTCTGCA	CGACAAGTAC	CCGGACCTCA	ACGAGTCGCG	TGCGTTCGAC	150
CAGATCGACA	ACGCTCCCGA	AGAGCGTCAG	CGCGGTATCA	CCATCAACAT	200
CTCCACGTG	GAGTACCAGA	CCGAGAAGCG	GCACTACGCC	CACGTCGACG	250
CTCCTGGTCA	CGCTGACTAC	ATCAAGAAC			279

## 2) INFORMATION FOR SEQ ID NO: 2267

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

1162

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria polysaccharea*  
 (B) STRAIN: ATCC 43768

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2267

```

ATGGCTAAGG AAAAATTCGA ACGTAGCAAA CCGCACGTAA ACGTTGGCAC      50
CATCGGTCAC GTTGACCATG GTAAAACCAC TCTGACTGCT GCTTTGACTA     100
CTATTTTGGC TAAAAAATTC GGCGGTGCTG CAAAAGCTTA CGACCAAATC     150
GACAACGCAC CCGAAGAAAA AGCACGCGGT ATTACCATTA ACACCTCGCA     200
CGTAGAATAC GAAACCGAAA CCCGCCACTA CGCACACGTA GACTGCCCCG      250
GTCACGCCGA CTACGTTAAA AAC                                     273
  
```

## 2) INFORMATION FOR SEQ ID NO: 2268

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*  
 (B) STRAIN: ATCC 14990

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2268

```

ATGGCAAAAG AAAAATTTGA TCGCTCAAAA GAACATGCCA ATATTGGTAC      50
TATCGGTCAC GTTGACCATG GTAAAACAAC TTAAACAGCT GCTATCGCAA     100
CTGTATTAGC TAAAAATGGT GACACTGTTG CACAATCATA CGATATGATT     150
GACAACGCTC CAGAAGAAAA AGAACGTGGT ATTACAATCA ATACTGCACA     200
TATCGAATAC CAAACTGACA AACGTCATA TGCTCACGTT GACTGCCCCAG     250
GACACGCTGA CTATGTTAAA AAC                                     273
  
```

## 2) INFORMATION FOR SEQ ID NO: 2269

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*  
 (B) STRAIN: ATCC 29970

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2269

ATGGCAAAAG	AAAAATTTGA	TCGCTCAAAA	GAACATGCCA	ATATTGGTAC	50
TATCGGTCAC	GTTGACCATG	GTAAACTAC	TTTAACAGCT	GCTATCGCAA	100
CTGTATTAGC	TAAAAATGGT	GACACTGTAG	CACAATCATA	TGACATGATT	150
GACAACGCTC	CAGAAGAAAA	AGAACGTGGT	ATCACAATCA	ATACTGCACA	200
CATCGAGTAT	CAAACTGACA	AACGTCATA	TGCTCACGTT	GACTGCCCAG	250
GACACGCTGA	CTATGTTAAA	AAC			273

## 2) INFORMATION FOR SEQ ID NO: 2270

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aeromonas hydrophila*
- (B) STRAIN: ATCC 7966

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2270

CGATCCTGGT	AGTAGCAGCG	ACTGACGGCC	CGATGCCGCA	GACTCGTGAG	50
CACATCCTGC	TGGGTCGTCA	GGTAGGCGTT	CCGTACATCA	TCGTGTTTCAT	100
GAACAAGTGT	GACATGGTAG	ATGACGAAGA	GCTGCTGGAA	CTGGTCGAGA	150
TGGAAGTTCG	CGAACTGCTG	TCCGAGTACG	ACTTCCCGGG	TGATGACCTG	200
CCGGTAGTCC	GTGGTTCYGC	ACTGAAAGCG	CTGGAAGGCG	AAGCTCAGTG	250
GGAAGAGAAG	ATCCTGGAAC	TGGCTGGCCA	CCTGGACACC	TACATTCCGG	300
AGCCGGAGCG	TGCCATCGAC	CTGCCGTTCC	TGATGCCTAT	CGAAGACGTA	350
TTCTCCATCG	CTGGCCGYGG	TACCGTAGTG	ACCGGTCGTG	TAGAGCGCGG	400
TATCGTCAAA	GTTGGTGAAG	AAGTGGAAAT	CGTKGGTATC	AAAGATACCA	450
CCAAGACCAC	CTGTACCGGC	GTTGAAATGT	TCCGCAAAC	GCTGGACGAA	500
GGTCGTGCAG	GCGAGAACAT	CGGTGCACTG	CTGCGTGGCG	TGAAGCGTGA	550
AGACGTAGAG	CGTGGTCAGG	TACTGGCCAA	GCCGGGCACC	ATCAAGCCGC	600
ACACCAAGTT	YGAATCTGAA	GTGTACGTGC	TGTCCAAAGA	AGAAGGTGGT	650
CGTCATACCC	CGTTCTTCAA	AGGCTACCGT	CCGCAGTTCT	ACTTCCGTAC	700
TACCGACGTG	ACCGGTACCA	TCGAACTGCC	GGAAGGCGTA	GAGATGGTAA	750
TGCCGGGCGA	CAACATCAAG	ATGGTTGTTA	CCCTGATTGC	GCCGATCGCG	800
ATGGACGACG	GC				812

## 2) INFORMATION FOR SEQ ID NO: 2271

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bilophila wadsworthia*



(B) STRAIN: ATCC 49260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2271

CGACGGTCCC	ATGCCCCAGA	CCCGTGAGCA	CATCCTGCTC	GCCCGTCAGG	50
TCGGCGTGCC	TCACCTCGTC	GTGTTCATGA	ACAAGTGTGA	CCTCGTCGAC	100
GACCCCGAAC	TGCTCGAACT	CGTCGAAATG	GAAGTCCGCG	AACTGCTGAG	150
CTCCTACGGC	TACCCCGGCG	ATGAAATCCC	GGTTGTCCGC	GGTTCCGCTC	200
TGAAGGCTCT	GGAATCCGAT	AGCGCTGATT	CCCCTGACGC	CCAGTGCGTG	250
CTCGAACTGC	TCGCCGCTTG	CGACAGCTAC	TTCCCGGATC	CGGTCCGCGA	300
AACCGACAAG	CCCTTCCTGA	TGCCCATCGA	AGACGTGTTC	TCCATCTCCG	350
GCCGCGGTAC	CGTGGTCACC	GGTCGTGTGG	AACGTGGCAT	CATCAAGGTC	400
GGCGAAGAAG	TCGAAATCGT	GGGTATCCGT	CCCACCGTGA	AGACGACCTG	450
CACCGGCGTC	GAAATGTTCC	GCAAGCTGCT	CGATCAGGGC	CAGGCCGGCG	500
ACAACATCGG	CGTCTGCTC	CGCGGCACGA	AGCGTGACGA	AGTGAACGC	550
GGCCAGGTTT	TCGCCGCTCC	CAAGAGCATC	ACGCCCCACA	AGAAGTTCAA	600
GGCTGAAGTG	TACGTTCTGT	CCAAGGAAGA	AGGCGGCCGC	CATACCCCGT	650
TCTTCACCGG	CTATCGTCCT	CAGTTCTACT	TCCGTACCAC	CGACATCACC	700
GGTATCATCG	CTCTTGAAGA	AGGCGTTGAA	ATGGTTATGC	CCGGCGATAA	750
CGTACCTTT	AATGTCGAGC	TCATTACCC	CATCGCCATG	GAAAAGGGC	799

2) INFORMATION FOR SEQ ID NO: 2272

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 786 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Brevundimonas diminuta*
- (B) STRAIN: ATCC 11568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2272

GATCCTGGTG	TGCTCGGCCG	CTGACGGCCC	GATGCCGCAG	ACCCGCGAGC	50
ACATCCTGCT	GTCGCGTCAG	GTCGGCGTTC	CGGCGCTGGT	GGTGTTCTTG	100
AACAAGGTCG	ACATGGTCGA	CGACGAGGAR	CTGCTGGAGC	TGGTCGAGAT	150
GGAAGTGCGC	GAGCTGCTGA	GCTCGTACCA	GTTCCCGGGC	GACGACATCC	200
CGGTGGTCAA	GGGCTCGGCC	CTGGCCGCGG	TGGAGGATCG	CGACCCGCAC	250
ATCGGCGCCG	AGCGCGTTCT	GGAGCTGATG	GCGGCGGTCT	ACAGCTACAT	300
CCCGCAGCCG	GAACGTCCGA	TCGACATGCC	GTTCTTGATG	CCGGTGGAAG	350
ACGTGTTCTC	GATCTCGGGC	CGCGGCACCG	TGGTGACGGG	TCGCGTCGAG	400
CGCGGCGTCG	TCAAGGTCGG	TGAAGAAGTC	GAAATCGTCG	GCATCCGTCC	450
GGTTCAGAAG	ACGACCTGCA	CGGGCGTCGA	AATGTTCCGC	AAGCTGCTGG	500
AYCAGGGTCA	RGCCGGCGAC	AACGTGGGCG	TGCTGCTGCG	CGGCACCAAG	550
CGTGAAGACG	TCGAGCGCGG	CCAGGTGCTG	TGCAAGCCGG	GTTTCGATCAC	600
CCCGCACACC	AAGTTCGTGG	CTGAAGCCTA	CATCCTGAAC	AAGGAAGAAG	650
GCGGCCGTCA	CACGCCGTTC	TTCACGAACT	ACCGTCCGCA	GTTCTACTTC	700
CGCACGACGG	ACGTGACCGG	CATCGTGCGC	CTGAAGGAAG	GCGTCGAGAT	750
GATCATGCCG	GGCGACAACG	CCGAGCTGGA	CGTCGA		786

## 2) INFORMATION FOR SEQ ID NO: 2273

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
- (B) STRAIN: LSPQ 2583

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2273

GCTATTATGG	CTGGATTACT	ATCCAATACG	CTATCCAAGA	ATCCCGTAAC	50
GTACCTGCCG	TCAAATCGCT	GGAAGCAGTC	GGATTAGATA	ATTCATTGAA	100
ATTCCTCAAT	GGCCTTG GTA	TCAATTATCC	TGAGATGCAT	TATTCTAATG	150
CGATTTCAAG	TAATACAAGC	GAATCTGGTA	ACCAATACGG	AGCAAGTAGC	200
GAAAAAATGG	CTGCCGCTTA	CGCTGCCTTT	GCTAATGGCG	GTACATATTA	250
CAAACCGCAA	TACGTCAACC	GAGTTGTCTT	TAGCGACGGT	ACAGAAAAAG	300
TCTTTTCAAA	TGGCGGATCA	AAAGCCATGA	AAGAGACGAC	AGCCTACATG	350
ATGACAGACA	TGATGAAGAC	CGTTCTTCAG	TCTGGAAGTG	GTACCAATGC	400
TGCAATCCCA	GGAGTTTATC	AAGCAGGTAA	AACTGGTACT	TCCAACATATG	450
CAGATGATGA	GCTAGAGAAG	TTGACAAAAC	CTTATTACAG	TTCTAGCATT	500
GTCACACCAG	ACGAACTATT	TGTTGGCTAT	ACTCCACAAT	ACTCTATGGC	550
TGTTTGGACA					560

## 2) INFORMATION FOR SEQ ID NO: 2274

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
- (B) STRAIN: ATCC 49456

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2274

GCTACTTTGG	AAACATTACT	GTCCAATATG	CTCTTCAACA	ATCACGTAAT	50
GTCACAGCCG	TTGAAACTTT	GAATAAGGTC	GGTCTAGATA	AGGCTAAAGC	100
CTTCCTTAAT	GGGCTTG GTA	TTGATTATCC	AAGCATGCAT	TATGCAAACG	150
CCATTTCAAG	TAATACAAC T	GAATCCAACA	AAAAATACGG	TGCAAGTAGT	200
GAAAAAATGG	CTGCTGCCTA	CGCTGCTTTT	GCTAATGGTG	GTATTTACCA	250
CAAGCCAATG	TACATCAATA	AAATCGTCTT	TAGCGACGGT	AGTGAGAAAG	300
AATTTTCTGA	TGCCGGCACA	CGAGCTATGA	AAGAACTAC	TGCCTATATG	350
ATGACTGAAA	TGATGAAAAC	AGTCCTAGTA	TACGGTACCG	GACGTGGAGC	400
CTACCTACCA	TGGCTTCCAC	AAGCAGGTAA	GACAGGTACT	TCTAACTATA	450

CTGACGACGA	AATTGAAAAG	TATATCAAGA	ACACTGGCTA	CGTAGCCCCA	500
GATGAAATGT	TTGTAGGGTA	TACTCGTAA	TATGCAATGG	CTGTTTGGAC	550
A					551

## 2) INFORMATION FOR SEQ ID NO: 2275

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
- (B) STRAIN: ATCC 903

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2275

GCTATTATGG	CTGGATTACT	ATCCAATACG	CTATCCAAGA	ATCCCGTAAC	50
GTACCAGCCG	TCAAATCGCT	GGAAGCAGTC	GGATTAGATA	ATTCATTGAA	100
GTTCTTCAAT	GGCCTTGGTA	TTAATTACCC	TGAAATGCAT	TATTCTAATG	150
CGATTTCAAG	TAATACAAGC	GAATCTGGTA	ACCAATACGG	AGCAAGTAGC	200
GAAAAAATGG	CTGCCGCTTA	CGCTGCCTTT	GCTAATGGCG	GTACATATTA	250
CAAACCGCAA	TACGTCAACC	GAGTTGTCTT	TAGCGACGGT	ACAGAAAAAG	300
TCTTTTCAAA	TGGCGGATCA	AAAGCCATGA	AAGAAACGAC	AGCCTACATG	350
ATGACAGACA	TGATGAAGAC	CGTTCTTCAA	TCTGGAAGTG	GTACCAATGC	400
TGCAATTCCA	GGAGTCTATC	AAGCAGGTAA	AACCGGCACT	TCCAACTATG	450
CAGATGATGA	ACTAGAGAAG	TTGACAAAAC	CTTATTACAG	TTCTAGCATT	500
GTCACACCAG	ACGAGCTGTT	TGTTGGCTAC	ACTCCACAGT	ACTCTATGGC	550
TGTTTGGACA					560

## 2) INFORMATION FOR SEQ ID NO: 2276

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus oralis*
- (B) STRAIN: ATCC 35037

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2276

TTATTTTGGG	AATATCACCA	TCCAATATGC	GCTCCAACAA	TCACGGAACG	50
TTACAGCCGT	AGAAACCTTG	AACAAAGTCG	GTTTGGATAG	AGCCAAGACC	100
TTCCTGAATG	GAATCGGTAT	TGACTATCCA	GATATGCACT	ATGCCAACGC	150
GATTTCAAGT	AATACGACTG	AGTCAAACAA	AAAGTACGGA	GCAAGTAGTG	200

AGAAAATGGC	TGCTGCTTAC	GCTGCTTTTG	CTAACGGTGG	TATCTACCAT	250
AAACCAATGT	ATATCAACAA	AATCGTCTTT	AGCGATGGTA	GCTCAAAAGA	300
ATACGCTGAT	CCTGGTACTC	GTGCCATGAA	AGAGACGACC	GCCTATATGA	350
TGACAGAAAT	GATGAAGACT	GTCTTGGCAT	ACGGAACGGG	TCGTGGTGCT	400
TATCTCCCTT	GGCTACCTCA	AGCTGGTAAG	ACTGGTACAT	CAAACCTATAC	450
AGATGATGAA	ATTGAAAAC	ACATCAAAAA	TACTGGTTAT	GTAGCCCCAG	500
ACGAAATGTT	TGTTGGTTAT	ACTCGCAAAT	ATTCAATGGC	TGTWTGGACA	550

## 2) INFORMATION FOR SEQ ID NO: 2277

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 35401

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2277

GCTCCTATCT	GGATTATGCG	ATGTCGGTCA	TTGTTGGCCG	TGCGCTGCCA	50
GATGTCCGAG	ATGGCCTGAA	GCCGGTACAC	CGTCGCGTAC	TTTACGCCAT	100
GAACGTACTA	GGCAATGACT	GGAACAAAGC	CTATAAAAAA	TCTGCCCGTG	150
TCGTTGGTGA	CGTAATCGGT	AAATACCATC	CCCATGGTGA	CTCGGCGGTC	200
TATGACACGA	TCGTCCGCAT	GGCGCAGCCA	TTCTCGCTGC	GTTATATGCT	250
GGTAGACGGT	CAGGGTAACT	TCGGTTCTAT	CGACGGCGAC	TCTGCGGCGG	300
CAATGCGTTA	TACGGAAATC	CGTCTGGCGA	AAATTGCCCA	TGAACTGATG	350
GCCGAT					356

## 2) INFORMATION FOR SEQ ID NO: 2278

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 23511

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2278

CTCTTATCTG	GATTATGCGA	TGTCGGTCAT	TGTTGGCCGC	GCGCTGCCGG	50
ATGTCCGAGA	TGGCCTGAAG	CCGGTACACC	GTCGCGTACT	TTACGCCATG	100
AACGTATTGG	GCAATGACTG	GAACAAAGCC	TACAAAAAAT	CAGCCCGTGT	150
CGTTGGTGAC	GTGATCGGTA	AATACCACCC	GCACGGCGAC	TCCGCGGTAT	200

ATGACACCAT	CGTTCGTATG	CCCCAGCCGT	TCTCGCTGCG	CTACATGCTG	250
GTGGATGGCC	AGGGGAACTT	CGGTTCAATC	GACGGCGACT	CCGCCGCGGC	300
AATGCGTTAT	ACGGAAATCC	GTCTGGCGAA	AATTGCTCAC	GAAGTGA	347

## 2) INFORMATION FOR SEQ ID NO: 2279

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 43886

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2279

AGAGCTCCTA	TCTGGATTAT	GCGATGTCGG	TCATTGTTGG	CCGTGCGCTG	50
CCAGATGTCC	GAGATGGCCT	GAAGCCGGTA	CACCGTCGCG	TACTTTACGC	100
CATGAACGTA	CTAGGCAATG	ACTGGAACAA	AGCCTATAAA	AAATCTGCCC	150
GTGTCGTTGG	TGACGTAATC	GGTAAATACC	ATCCCCATGG	TGACTCGGCG	200
GTCTATGACA	CGATCGTCCG	CATGGCGCAG	CCATTCTCGC	TGCGTTATAT	250
GCTGGTAGAC	GGTCAGGGTA	ACTTCGGTTC	TATCGACGGC	GACTCTGCGG	300
CGGCAATGCG	TTATACGGAA	ATCCGTCTGG	CGAAAATTGC	CCATGAACTG	350
ATGGCCGATC	TC				362

## 2) INFORMATION FOR SEQ ID NO: 2280

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 25922

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2280

CTCCTATCTG	GATTATGCGA	TGTCGGTCAT	TGTTGGCCGT	GCGCTGCCAG	50
ATGTCCGAGA	TGGCCTGAAG	CCGGTACACC	GTCGCGTACT	TTACGCCATG	100
AACGTACTAG	GCAATGACTG	GAACAAAGCC	TATAAAAAAT	CTGCCCGTGT	150
CGTTGGTGAC	GTAATCGGTA	AATACCATCC	CCATGGTGAC	TCGGCGGTTT	200
ATGACACGAT	CGTCCGTATG	GCGCAGCCAT	TCTCGCTGCG	TTACATGCTG	250
GTAGACGGTC	AGGGTAACTT	CGGTTCCATC	GACGGCGACT	CTGCGGCGGC	300
AATGCGTTAT	ACGGAAATCC	GTCTGGCGAA	AATTGCCCCAT	GAAGTGATGG	350
CCGATCTC					358

## 2) INFORMATION FOR SEQ ID NO: 2281

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2281

CCCCCAGCTG GCGGGCGGTA TCGATGGGGG

30

## 2) INFORMATION FOR SEQ ID NO: 2282

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2282

AGRRGCIMAR ATGTATGA

18

## 2) INFORMATION FOR SEQ ID NO: 2283

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2283

ATITATGAYG GKITTCAGAG GC

22

## 2) INFORMATION FOR SEQ ID NO: 2284

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2284

TCTGWGTRAC IGGYTCKGAG A

21

2) INFORMATION FOR SEQ ID NO: 2285

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2285

CMCCICCWGG TGGWGAWAC

19

2) INFORMATION FOR SEQ ID NO: 2286

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2286

AGTTGCTGTA TTAGGAAATG

20

2) INFORMATION FOR SEQ ID NO: 2287

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2287

TCGAAGTTGC TGTATTAGGA

20

2) INFORMATION FOR SEQ ID NO: 2288

1171

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1240 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
- (B) STRAIN: BM4339

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2288

TAGAAGCTGG	CTCGTTTTTT	TATAAATAAG	TTATTCGTTT	ATTTTTGTTT	50
TGTGCTAAAA	TATGAGAGTA	AATCACTGAA	CGATTTAGAA	TACAGGAGGA	100
CAATCTTTTG	AAGATTACTT	TACTATATGG	CGGACGCAGC	GCAGAGCAGA	150
GCATGAAGTG	TCCATTCTTT	CCGCATTTTC	AGTTTTAAAT	GCCATTTATT	200
ATAATTATTA	CCAAGTTCAA	CTCGTATTTA	TTACAAAAGA	AGGACAATGG	250
GTCAAAGGTC	CATTACTAAC	AGAAAAACCT	GCCAGCAAAG	ATGTCTTGCA	300
TCTTTCATGG	GACCCAAGTG	GACAGACAGA	GGAAGGCTTT	ACAGGAAAAG	350
TGATCAATCC	GGGCGAAATC	AAAGAAGAAG	GAGCCATCGT	TTTTCAGTT	400
TTACATGGGC	CAAACGGGGA	AGATGGAACG	ATCCAAGGCT	TCTTAGAGAC	450
ATTGAATATG	CCTTATGTCT	GCGCAGGCGT	ATTGACCAGT	GCATGTGCCA	500
TGGATAAAAT	CATGACCAAG	TATATTTTAC	AAGCTGCTGG	TGTGCCGCAA	550
GTTCCCTTATG	TACCACTACT	TAAGAATCAA	TGGAAAGAAA	ATCCTAAAAA	600
AGTATTTGAT	CAATGTGAAG	GTTCTTTGCT	TTATCCGATG	TTTGTCAAAC	650
CGGCGAATAT	GGGTCTAGT	GTCGGCATT	CAAAAGCAGA	AAACCGAGAA	700
GAGCTGCAAA	ATGCTTTAGC	AACAGCCTAT	CAGTATGATT	CTCGAGCAAT	750
CGTTGAACAA	GGAATTGAAG	CGCGCGAAAT	CGAAGTTGCT	GTATTAGGAA	800
ATGAAGACGT	TCGGACGACT	TTGCCTGGTG	AAGTCGTAAA	AGACGTAGCA	850
TTCTATGATT	ATGAAGCAAA	ATATATCAAT	AATAAAATCG	AAATGCAGAT	900
TCCAGCCGAA	GTGCCAGAAG	AAGTTTATCA	AAAAGCGCAA	GAGTACGCGA	950
AGTTAGCTTA	CACGATGTTA	GGTGGAAGCG	GATTGAGCCG	GTGCGATTTC	1000
TTTTTGACAA	ATAAAAATGA	ATTATTCCTG	AATGAATTAA	ACTCTATGCC	1050
AGGATTTACG	GAGTTCAGTA	TGTACCCACT	CTTATGGGAA	AATATGGGCT	1100
TGAAATACGG	TGATTTGATT	GAAGAACTGA	TCCAGTTAGG	AATGAATCGA	1150
TACCATCAGC	GTCAATCTTT	TTTTGAAAAA	AATGAATAAA	GAGAAATAAA	1200
GAAGAGGCTG	GAGTGATTGC	GTAACGCGCT	TCATTCTAGC		1240

## 2) INFORMATION FOR SEQ ID NO: 2289

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2289

CACCGAAGAA GATGAAAAAA

20



## 2) INFORMATION FOR SEQ ID NO: 2290

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2290

TGGCACCGAA GAAGATGA

18

## 2) INFORMATION FOR SEQ ID NO: 2291

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2291

ATTTTGGCAC CGAAGAAGA

19

## 2) INFORMATION FOR SEQ ID NO: 2292

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2292

GAATCGGCAA GACAATATG

19

## 2) INFORMATION FOR SEQ ID NO: 2293

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1032 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

(B) STRAIN: BM4147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2293

ATGAATAGAA	TAAAAGTTGC	AATACTGTTT	GGGGGTTGCT	CAGAGGAGCA	50
TGACGTATCG	GTAAATCTG	CAATAGAGAT	AGCCGCTAAC	ATTAATAAAG	100
AAAAATACGA	GCCGTTATAC	ATTGGAATTA	CGAAATCTGG	TGTATGGAAA	150
ATGTGCGAAA	AACCTTGCGC	GGAATGGGAA	AACGACAATT	GCTATTTCAGC	200
TGTACTCTCG	CCGGATAAAA	AAATGCACGG	ATTACTTGTT	AAAAAGAACC	250
ATGAATATGA	AATCAACCAT	GTTGATGTAG	CATTTTCAGC	TTTGCATGGC	300
AAGTCAGGTG	AAGATGGATC	CATACAAGGT	CTGTTTGAAT	TGTCCGGTAT	350
CCCTTTTGTA	GGCTGCGATA	TTCAAAGCTC	AGCAATTTGT	ATGGACAAAT	400
CGTTGACATA	CATCGTTGCG	AAAAATGCTG	GGATAGCTAC	TCCCGCCTTT	450
TGGGTTATTA	ATAAAGATGA	TAGGCCGGTG	GCAGCTACGT	TTACCTATCC	500
TGTTTTTGTT	AAGCCGGCGC	GTTCAGGCTC	ATCCTTCGGT	GTGAAAAAAG	550
TCAATAGCGC	GGACGAATTG	GACTACGCAA	TTGAATCGGC	AAGACAATAT	600
GACAGCAAAA	TCTTAATTGA	GCAGGCTGTT	TCGGGCTGTG	AGGTCGGTTG	650
TGCGGTATTG	GGAAACAGTG	CCGCGTTAGT	TGTTGGCGAG	GTGGACCAAA	700
TCAGGCTGCA	GTACGGAATC	TTTCGTATTC	ATCAGGAAGT	CGAGCCGGAA	750
AAAGGCTCTG	AAAACGCAGT	TATAACCGTT	CCCGCAGACC	TTTCAGCAGA	800
GGAGCGAGGA	CGGATACAGG	AAACGGCAAA	AAAAATATAT	AAAGCGCTCG	850
GCTGTAGAGG	TCTAGCCCGT	GTGGATATGT	TTTTACAAGA	TAACGGCCGC	900
ATTGTACTGA	ACGAAGTCAA	TACTCTGCCC	GGTTTCACGT	CATACAGTCG	950
TTATCCCCGT	ATGATGGCCG	CTGCAGGTAT	TGCACTTCCC	GAAGTGATTG	1000
ACCGCTTGAT	CGTATTAGCG	TTAAAGGGGT	GA		1032

## 2) INFORMATION FOR SEQ ID NO: 2294

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2294

AAACGAGGAT GATTTGATTG

20

## 2) INFORMATION FOR SEQ ID NO: 2295

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2295

TTGAGCAAGC GATTTCGG

18

## 2) INFORMATION FOR SEQ ID NO: 2296

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1029 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
- (B) STRAIN: V583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2296

ATGAATAAAA	TAAAAGTCGC	AATTATCTTC	GGCGGTTGCT	CGGAGGAACA	50
TGATGTGTCTG	GTAAAATCCG	CAATAGAAAT	TGCTGCGAAC	ATTAATACTG	100
AAAAATTCTGA	TCCGCACTAC	ATCGGAATTA	CAAAAAACGG	CGTATGGAAG	150
CTATGCAAGA	AGCCATGTAC	GGAATGGGAA	GCCGATAGTC	TCCCCGCCAT	200
ATTCTCCCCG	GATAGGAAAA	CGCATGGTCT	GCTTGTCATG	AAAGAAAGAG	250
AATACGAAAC	TCGGCGTATT	GACGTGGCTT	TCCCGGTTTT	GCATGGCAAA	300
TGCGGGGAGG	ATGGTGCGAT	ACAGGGTCTG	TTTGAATTGT	CTGGTATCCC	350
CTATGTAGGC	TGCGATATTC	AAAGCTCCGC	AGCTTGCAATG	GACAAATCAC	400
TGGCCTACAT	TCTTACAAAA	AATGCGGGCA	TCGCCGTCCC	CGAATTTCAA	450
ATGATTGAAA	AAGGTGACAA	ACCGGAGGCG	AGGACGCTTA	CCTACCCTGT	500
CTTTGTGAAG	CCGGCACGGT	CAGGTTCTGTC	CTTTGGCGTA	ACCAAAGTAA	550
ACAGTACGGA	AGAACTAAAC	GCTGCGATAG	AAGCAGCAGG	ACAATATGAT	600
GGAAAAATCT	TAATTGAGCA	AGCGATTTCG	GGCTGTGAGG	TCGGCTGCGC	650
GGTCATGGGA	AACGAGGATG	ATTTGATTGT	CGGCGAAGTG	GATCAAATCC	700
GGTTGAGCCA	CGGTATCTTC	CGCATCCATC	AGGAAAACGA	GCCGGAAAAA	750
GGCTCAGAGA	ATGCGATGAT	TATCGTTCCA	GCAGACATTC	CGGTGAGGA	800
ACGAAATCGG	GTGCAAGAAA	CGGCAAAGAA	AGTATATCGG	GTGCTTGAT	850
GCAGAGGGCT	TGCTCGTGTT	GATCTTTTTT	TGCAGGAGGA	TGGCGGCATC	900
GTTCTAAACG	AGGTCAATAC	CCTGCCCCGT	TTTACATCGT	ACAGCCGCTA	950
TCCACGCATG	GCGGCTGCCG	CAGGAATCAC	GCTTCCCGCA	CTAATTGACA	1000
GCCTGATTAC	ATTGGCGATA	GAGAGGTGA			1029

## 2) INFORMATION FOR SEQ ID NO: 2297

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2297

TTCAGGAGGG GGATCGC

17